



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179839

TO: Stephen Kapushoc
Location: REM/3A60/2C70
Art Unit: 1634
Wednesday, February 22, 2006
Case Serial Number: 10/785981

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

*swine chip
requested working folder
2-23-06*

This Page Blank (uspto)

STIC-Biotech/ChemLib

199839

From: Kapushoc, Stephen T.
Sent: Thursday, February 16, 2006 4:32 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search for 10/785,981

Please search SEQ ID NOs: 1, 2, 3, 4, 5 for application 10/785,981

Thanks,
Steve

Stephen Kapushoc
Art Unit 1634 - USPTO
Tel: 571-272-3312
Office: REM 3A60
Mailbox: REM 2C70

RECEIVED
FEB 15 2006
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 392.58 Seconds
(without alignments)
9396.598 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccagcaatactatgt.....tgcaccatgaagctttgagt 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	1588	9 BC004067	BC004067 Mus muscu
2	660	100.0	1754	9 BC005660	BC005660 Mus muscu
3	660	100.0	1761	9 BC018485	BC018485 Mus muscu
4	660	100.0	1771	9 BC092053	BC092053 Mus muscu
5	660	100.0	1778	9 BC018223	BC018223 Mus muscu
6	658.4	99.8	1736	9 BC004005	BC004005 Mus muscu
7	658.4	99.8	1756	9 BC092276	BC092276 Mus muscu
8	656.8	99.5	1760	9 BC095965	BC095965 Mus muscu
9	656.8	99.5	1779	9 BC083069	BC083069 Mus muscu
10	653.6	99.0	181014	9 AL840626	AL840626 Mouse DNA
11	647.2	98.1	1722	6 AX306117	AX306117 Sequence
12	647.2	98.1	1722	9 MUSEFTU	M22432 Mus musculu
13	629.6	95.4	145253	9 AC138173	AC138173 Mus muscu
14	629.6	95.4	186564	9 AC119816	AC119816 Mus muscu
15	628.2	95.2	214658	9 AC133509	AC133509 Mus muscu
16	626.4	94.9	1714	9 RNEP1A	X63561 R.norvegicu
17	626.4	94.9	1737	9 RNEP1AA	X61043 R.norvegicu
18	626.4	94.9	1746	9 BC091297	BC091297 Rattus no

19	626.4	94.9	1771	9 BC063162	BC063162 Rattus no
20	626.4	94.9	1775	9 BC072542	BC072542 Rattus no
21	626.4	94.9	182416	9 AC099724	AC099724 Mus muscu
22	626.4	94.9	192528	9 AC124512	AC124512 Mus muscu
23	626.4	94.9	233219	14 AC136572	AC136572 Rattus no
24	626.4	94.2	250880	9 AC102040	AC102040 Mus muscu
c	625.4	94.8	136258	14 AC166149	AC166149 Mus muscu
25	625.4	94.8	179579	14 AC166748	AC166748 Mus muscu
c	625.4	94.8	208266	14 AC110913	AC110913 Mus muscu
27	624.8	94.7	1704	9 MMEF1A	X13661 Mouse mRNA
c	621.8	94.2	150755	9 AC154274	AC154274 Mus muscu
30	621.6	94.2	1404	9 RAEF1AX	L10339 Rat elongat
31	614.4	93.1	175370	14 AC145861	AC145861 Pan trogl
32	614.4	93.1	175641	9 AC147556	AC147556 Mus muscu
c	614.4	93.1	181867	14 AC134666	AC134666 Mus muscu
34	614.4	93.1	222816	14 AC161170	AC161170 Mus muscu
c	608.8	92.2	183837	9 AC100406	AC100406 Mus muscu
c	608.8	92.2	287411	14 AC154479	AC154479 Mus muscu
37	605.6	91.8	1722	9 CRUEF1A	D00522 Cricetulus
38	596	90.3	1515	4 OCEF1A	X62245 O.cuniculus
c	592.6	89.8	242590	14 OC094797	OC094797 Rattus no
40	592.6	89.8	247086	14 AC134118	AC134118 Rattus no
c	590.4	89.5	230228	14 AC116224	AC116224 Rattus no
c	590	89.4	161222	9 AC154254	AC154254 Mus muscu
44	590	89.4	200115	14 AC154774	AC154774 Mus muscu
c	588.4	89.2	254169	14 AC127720	AC127720 Rattus no

ALIGNMENTS

RESULT 1

BC004067

LOCUS

DEFINITION

Mus musculus eukaryotic translation elongation factor 1 alpha 1, mRNA (CDNA clone MGC:8209 IMAGE:3590965), complete cds.

ACCESSION

BC004067

VERSION

BC004067.1

KEYWORDS

MGC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 1588)

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dicken,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butler,L.Y.S., Krzyzanski,M.I., Skalek,U., Smallos,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED

12477932

REFERENCE

2 (bases 1 to 1588)

AUTHORS

Director MGC Project.

TITLE

Direct Submission

JOURNAL

Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC004067 1588 bp mRNA linear ROD 07-SEP-2004

Mus musculus eukaryotic translation elongation factor 1 alpha 1, mRNA (CDNA clone MGC:8209 IMAGE:3590965), complete cds.

BC004067

BC004067.1 GI:13278545

MGC.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 1588)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dicken,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butler,L.Y.S., Krzyzanski,M.I., Skalek,U., Smallos,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1588)

Director MGC Project.

Direct Submission

Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-x@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 11 Row: C Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

```

FEATURES             Location/Qualifiers
  1..1598
     /organism="Mus musculus"
     /mol_type="mRNA"
     /strain="Czech II"
     /db_xref="taxon:10090"
     /clone="MGC:8209 IMAGE:3590965"
     /tissue_type="Mammary tumor metastatized to lung. Tumor
arose spontaneously from a senescent normal mammary
(cloneal) outgrowth infected with the virus MMTV."
     /clone_lib="NCI CGAP_Lu29"
     /lab_host="DH10B"
     /note="Vector: pCMV-SPORT6"
  1..1598
     /gene="Eef1a1"
     /note="synonyms: MGC18758, MGC27859, MGC7551, MGC8115,
MGC8209"
     /db_xref="GeneID:13627"
     /db_xref="MGI:1096881"
     58..1446
     /gene="Eef1a1"
     /codon_start=1
     /product="eukaryotic translation elongation factor 1 alpha
1"
     /protein_id="AAH04087.1"
     /db_xref="GI:13278546"
     /db_xref="GeneID:13627"
     /db_xref="MGI:1096881"
     /translation="MGKEKTHINIVIGHVDSKSTTTGHLIVKCGGIDKRTIEKPEK
EABMGKGSFYAAVLDKLKAEERGITIDISLWKFTSKYVYTIIDAPGHRDFIKNTP
ITGTSQADCAVLVAAGGSGFAGISKNGQTRHEALAYTLGVKQLIIVGNKMDSTETP
PYQKSEETIIVKEVSTYIKKIGNPDTVAFPVIGSMGDNMLPESAMPFGWKTIVR
KDSASGTEILADCLDCLPTPTKPLQDVYKIGITGVPGVRGTVGLVKPQM
VVFAPVNTVHKVSGVBMHHEALSEALPGDNVFNKVSVDVVRGNVAGDSKNDP
MEAGFTAQVITLNVKPGQISAGVAVLDDTAHIACKFAELKEKIDRRSGKLEIDGPK
FLKSGDAAIVDMVPGKPMCVESPSDYPPLGRPAVRDMRQTVAGVVIKAVDKKAAGAK
VTKGDEKQAYAV"

```

ORIGIN					
			Query Match	100.0%; Score 660; DB 9;	Length 1588;
			Best Local Similarity	100.0%; Pred. No. 6.6e-186;	
			Matches 660; Conservative	0; Mismatches	0; Indels
				0; Gaps	0;
Qy	1	GAGACGAGCAAAATCTATGTGCACCATCATTTGATGCCCGCAGGACACAGAGACTTTCATCAA	60		
Dd	298	GAGACCAGCAAAATCTATGTGCACCATCATTTGATGCCCGCAGGACACAGAGACTTTCATCAA	357		
Qy	61	AACATGATTACAGGCACATCCCAGGCTGACTGTCTGCTCTGATTGTGCTGCTGGTGTT	120		
Dd	358	AACATGATTACAGGCACATCCCAGGCTGACTGTCTGCTCTGATTGTGCTGCTGGTGTT	417		
Qy	121	GGTGAATTTGAAGCTGTGTATCTCCAAGAACGGGGCAGACCCCGCAGCATGCTCTTCTGGCT	180		

[illegible]

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 560.102 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccagcaatactatgt.....tgaccatgaagcttgagt 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	660	14 ADZ89038	Adz89038 Pig growt
2	660	100.0	660	14 ADZ79331	Adz79331 Swine gro
3	660	100.0	660	14 ADZ77168	Adz77168 Pig growt
4	655.2	99.3	1722	10 ADF30645	Adf30645 Rat anglo
5	647.2	98.1	1722	6 ABI99778	Abi99778 Mouse isc
6	621.6	94.2	1404	10 ADS58712	Ads58712 Toxicity-
7	621.6	94.2	1404	13 ADVA1496	Adv41496 Rat cardi
8	581.6	88.1	1246	4 AAI22127	Aai22127 Probe #12
9	581.6	88.1	1246	4 ABA67206	Aba67206 Human foe
10	581.6	88.1	1246	4 AAI47423	Aai47423 Probe #15
11	581.6	88.1	1246	4 ABA49293	Aba49293 Human bre
12	581.6	88.1	1246	4 ABA34302	Aba34302 Probe #12
13	581.6	88.1	1246	4 AAK41382	Aak41382 Human bon
14	581.6	88.1	1246	4 AAK15648	Aak15648 Human bra
15	581.6	88.1	1246	4 ABS40975	Abs40975 Human liv
16	581.6	88.1	1246	5 ABS407827	Abs407827 Probe #78
17	581.6	88.1	1246	6 ABS15387	Abis15387 Human gen
18	581.6	88.1	1389	12 AD000457	Ado00457 Novel hum
19	581.6	88.1	1389	12 ADN98888	Adn98888 Novel hum

20	581.6	88.1	1494	6 ABL58971	AbL58971 Human tum
21	581.6	88.1	1506	11 ADI31952	Adi31952 Human cDN
22	581.6	88.1	1506	12 ADQ87715	Adq87715 Human tum
23	581.6	88.1	1506	13 ACQ84157	Acq84157 Human tum
24	581.6	88.1	1506	13 ACN18509	Acn18509 Tumour-as
25	581.6	88.1	1506	13 ADS84019	Ads84019 Human lym
26	581.6	88.1	1696	5 ABA82688	Aba82688 Elongatio
27	581.6	88.1	1696	8 ABX10398	Abx10398 DNA encod
28	581.6	88.1	1696	8 ACC46008	Acc46008 Human elo
29	581.6	88.1	1696	10 ADB98702	Adb98702 Human elo
30	581.6	88.1	1696	10 ADS82498	Ads82498 Human DNA
31	581.6	88.1	1744	13 ADR07233	Adr07233 Full leng
32	581.6	88.1	1833	8 ACF34510	Acf34510 Gene enco
33	581.6	88.1	1833	12 ADL35468	Adl35468 Human euk
34	581.6	88.1	1833	13 ADS88611	Ads88611 Human hou
35	581.6	88.1	1833	13 ADU60293	Adu60293 Housekeep
36	581.6	88.1	1837	12 ADJ62805	Adj62805 Human cDN
37	581.6	88.1	1837	12 ADF10528	Adf10528 Reference
38	581.6	88.1	1837	14 AEB03626	Aeb03626 Human gen
39	581.6	88.1	1837	14 AAI12888	Aai12888 Probe #28
40	581.6	88.1	1950	4 ABA54589	Aba54589 Human foe
41	581.6	88.1	1950	4 AAI34246	Aai34246 Probe #29
42	581.6	88.1	1950	4 ABA44138	Aba44138 Human bre
43	581.6	88.1	1950	4 ABA24374	Aba24374 Probe #28
44	581.6	88.1	1950	4 AAK28323	Aak28323 Human bon
45	581.6	88.1	1950	4 AAK28323	Aak28323 Human bon

ALIGNMENTS

RESULT 1

ADZ89038

ID ADZ89038 standard; DNA; 660 BP.

XX ADZ89038;

AC ADZ89038;

28-JUL-2005 (first entry)

Pig growth factor I (GF I) gene, seq id 1.

Growth; biochip; swine; hog raising; growth factor I; gene; ds.

Sub scrofa; Kagoshima Berkshire.

US2005112597-A1.

26-MAY-2005.

26-FEB-2004; 2004US-00785981.

24-NOV-2003; 2003KR-00083653.

(KIMC/) KIM C.

(YEOJ/) YEO J.

(LEEJ/) LEE J.

(SONG/) SONG Y.

(CHOK/) CHO K.

(CHUN/) CHUNG K.

(KIMI/) KIM I.

(JINS/) JIN S.

(PARK/) PARK S.

(JUNG/) JUNG J.

(LEEM/) LEE M.

(KWON/) KWON E.

(CHOE/) CHO E.

(CHOH/) CHO H.

(SHIN/) SHIN S.

(NAME/) NAM H.

(HONG/) HONG Y.

(HONG/) HONG S.

(KANG/) KANG Y.

(HAYY/) HA Y.

```
PA (ROUJ/) ROU J,
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX
XX WPI; 2005-403340/41.
XX
XX Functional cDNA chip useful for screening and function analysis of growth
PT specific genes according to breeds and tissues of swine, comprises
PT substrate and probe comprising growth specific genes in muscle and fat
PT tissues of swine.
XX
XX Claim 2; SEQ ID NO 1; 8pp; English.
XX
XX The invention relates to a functional cDNA chip (I) for screening and
CC function analysis of growth specific genes according to breeds and
CC tissues of swine, comprises a probe comprising growth specific genes in
CC muscle and fat tissues of swine, and a substrate on which the probe is
CC immobilized. Further disclosed is a kit (KI) useful for screening and
CC functional analysis of growth specific gene according to breeds and
CC tissues of swine, comprising (I) integrated in it, Cy5-dCTP or Cy3-dCTP
CC bound cDNA from RNA of the tissue to be screened, a fluorescence scanning
CC system, and a computer analysis system. (I) and (KI) are useful for
CC screening and function analysis of growth specific gene according to
CC breeds and tissues of swine. (II) is useful in the swine improvement and
CC breeding of a new breed, and in the hog raising industry. The current
CC sequence represents the pig growth factor I (GF I) gene.
XX
XX Sequence 660 BP; 178 A; 157 C; 166 G; 159 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 660; DB 14; Length 660;
Best Local Similarity 100.0%; Pred. No. 4.2e-193;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGACCGAATAACTATGTGACCATCATTTGATGCCCGGAGACACAGAGATTTCATCAA 60
Db 1 GAGACCGAATAACTATGTGACCATCATTTGATGCCCGGAGACACAGAGATTTCATCAA 60
Qy 61 AACATGATTACAGGCACATCCAGCGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AACATGATTACAGGCACATCCAGCGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 GGTGAATTTGAAGCTGTGATATCCAGAAACGGGAGAGCCCGGAGCATGCTCTCTGGCT 180
Db 121 GGTGAATTTGAAGCTGTGATATCCAGAAACGGGAGAGCCCGGAGCATGCTCTCTGGCT 180
Qy 181 TACACCTGGGTGGAACACAGCTGATTTGGTGTCAACAAATGGATTCACCGAGCCA 240
Db 181 TACACCTGGGTGGAACACAGCTGATTTGGTGTCAACAAATGGATTCACCGAGCCA 240
Qy 241 CCATACAGTCAGAGAGATACGAGGAATCTTAAAGGAAGTCACCACTACATTAAGAAA 300
Db 241 CCATACAGTCAGAGAGATACGAGGAATCTTAAAGGAAGTCACCACTACATTAAGAAA 300
Qy 301 ATTGGCTACAAACCTTGACACAGTAGCATTTCTGCCAATTTCTGGTTGGAATGGTGAAC 360
Db 301 ATTGGCTACAAACCTTGACACAGTAGCATTTCTGCCAATTTCTGGTTGGAATGGTGAAC 360
Qy 361 ATGCTGGAGCCAAAGTGTCTTAATATGCTTGGTTTCAAGGATGGAAGTCAACCGCAAGAT 420
Db 361 ATGCTGGAGCCAAAGTGTCTTAATATGCTTGGTTTCAAGGATGGAAGTCAACCGCAAGAT 420
Qy 421 GGCAGTGCAGTGCACACACCTGCTGGAAGCTTTGGATTTCTATCCACCACTTCGTT 480
Db 421 GGCAGTGCAGTGCACACACCTGCTGGAAGCTTTGGATTTCTATCCACCACTTCGTT 480
Qy 481 CCAACTGACAAAGCTCTCGGACTGCCCTCCAGGATGTCTATAAAATGGAGGATTGGC 540
Db 481 CCAACTGACAAAGCTCTCGGACTGCCCTCCAGGATGTCTATAAAATGGAGGATTGGC 540
```

```
Qy 541 ACTGTCCTCTGGGCGGAGTGGAGACTGGTCTCAAACTGCATGGTGGTTACCTTT 600
Db 541 ACTGTCCTCTGGGCGGAGTGGAGACTGGTCTCAAACTGCATGGTGGTTACCTTT 600
Qy 601 GCTCCAGTCAATGTAACAACACTGAAGTCAAGTCTGTTGAAATGCACCAATGAAGCTTTGAGT 660
Db 601 GCTCCAGTCAATGTAACAACACTGAAGTCAAGTCTGTTGAAATGCACCAATGAAGCTTTGAGT 660

RESULT 2
ADZ79331
ID ADZ79331 standard; cDNA; 660 BP.
XX
AC ADZ79331;
XX
XX 28-JUL-2005 (first entry)
XX
XX Swine growth factor GE-I cDNA for cDNA chip diagnostic method.
XX
XX biochip; screening; EST; expressed sequence tag; probe; muscle;
KW immobilization; gene expression; polymorphism; diagnosis;
KW animal breeding; growth factor; ss.
XX
XX Unidentified.
XX
XX US2005112602-A1.
XX
XX 26-MAY-2005.
XX
XX 27-FEB-2004; 2004US-00789723.
XX
XX 24-NOV-2003; 2003KR-00083651.
XX
XX (KIMC/) KIM C.
PA (YEOJ/) YEO J.
PA (LEEJ/) LEE J.
PA (SONG/) SONG Y.
PA (CHOK/) CHO K.
PA (CHUN/) CHUNG K.
PA (KIMI/) KIM I.
PA (JINS/) JIN S.
PA (PARK/) PARK S.
PA (JUNG/) JUNG J.
PA (LEEW/) LEE M.
PA (KWON/) KWON E.
PA (CHOE/) CHO E.
PA (CHOH/) CHO H.
PA (SHIN/) SHIN S.
PA (NAMH/) NAM H.
PA (HONG/) HONG Y.
PA (KANG/) KANG Y.
PA (HAYY/) HA Y.
PA (ROUJ/) ROU J.
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX
XX WPI; 2005-371656/38.
XX
XX New cDNA chip comprising a probe capable of detecting marker genes
PT specifically expressed in the muscle and fat tissues of swine, and a
PT substrate, useful for screening and function analysis of swine genes.
XX
XX Claim 9; SEQ ID NO 1; 15pp; English.
PS
XX The invention relates to a cDNA chip for screening and function analysis
CC of swine genes comprising a probe capable of detecting marker genes
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3910.41 Seconds
(without alignments)
7896.735 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccagcaataactatgt.....tgaccatgaagcttgagt 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	660	100.0	1700	BC092292	Mus muscu
2	656.8	99.5	673	BM945443	BM945443 UI-M-EMO-
3	656.8	99.5	678	CK788670	CK788670 HESC3_101
4	656.8	99.5	710	CB248368	CB248368 UI-M-FD0-
5	656.8	99.5	719	BM945776	BM945776 UI-M-EMO-
6	656.8	99.5	746	BM946759	BM946759 UI-M-EMO-
7	656.8	99.5	748	BQ042422	BQ042422 UI-M-EMO-
8	656.8	99.5	749	CA322009	CA322009 UI-M-EMO-
9	656.8	99.5	755	BQ444687	BQ444687 UI-M-EMO-
10	656.8	99.5	757	CF951596	CF951596 UI-M-HL0-
11	656.8	99.5	760	CF949906	CF949906 UI-M-HK0-
12	656.8	99.5	764	BQ177933	BQ177933 UI-M-HK0-
13	656.8	99.5	771	BQ177724	BQ177724 UI-M-EMO-
14	656.8	99.5	808	BQ571059	BQ571059 UI-M-EMO-
15	656.8	99.5	879	BUS12595	BUS12595 AGENCOURT
16	656.8	99.5	926	CA979421	CA979421 AGENCOURT
17	656.8	99.5	928	BQ922583	BQ922583 AGENCOURT
18	656.8	99.5	1111	BM453687	BM453687 AGENCOURT
19	656.8	99.5	1145	BM461263	BM461263 AGENCOURT
20	656.8	99.5	1153	BUS15235	BUS15235 AGENCOURT
21	656.8	99.5	1733	AK081725	AK081725 Mus muscu
22	656.8	99.5	1734	AK076696	AK076696 Mus muscu

23	656.8	99.5	1736	4	AK083361	AK083361 Mus muscu
24	655.8	99.4	690	7	CN456673	CN456673 UI-M-HP0-
25	655.8	99.4	701	7	CK780521	CK780521 UI-M-RA0-
26	655.8	99.4	708	6	CD364228	CD364228 UI-M-GL0-
27	655.8	99.4	748	6	CF734957	CF734957 UI-M-RA0-
28	655.2	99.3	686	7	CN455811	CN455811 UI-M-HP0-
29	655.2	99.3	693	7	CF951163	CF951163 UI-M-HL0-
30	655.2	99.3	879	6	CA978866	CA978866 AGENCOURT
31	655.2	99.3	931	6	CB183269	CB183269 AGENCOURT
32	655.2	99.3	1722	4	BC003969	BC003969 Mus muscu
33	655.2	99.3	1731	4	AK032914	AK032914 Mus muscu
34	654.8	99.2	745	3	BM946164	BM946164 UI-M-EMO-
35	654.2	99.1	749	6	CD364147	CD364147 UI-M-GL0-
36	654.2	99.1	749	7	CN456691	CN456691 UI-M-HP0-
37	654.2	99.1	943	5	BQ891120	BQ891120 AGENCOURT
38	653.8	99.1	760	6	CF731605	CF731605 UI-M-RA0-
39	653.8	99.1	776	7	CK780620	CK780620 UI-M-RA0-
40	653.6	99.0	781	3	BM945492	BM945492 UI-M-EMO-
41	653.2	99.0	725	6	CF731619	CF731619 UI-M-HL0-
42	653.2	99.0	803	7	CF950931	CF950931 UI-M-HL0-
43	652	98.8	910	6	CA978558	CA978558 AGENCOURT
44	651.8	98.8	745	2	BE911061	BE911061 601662158
45	651.6	98.7	795	5	BQ571020	BQ571020 UI-M-EMO-

ALIGNMENTS

RESULT 1
BC092292
LOCUS Mus musculus cdna clone IMAGE:5068840, containing frame-shift errors.
DEFINITION BC092292.1 GI:62185631
ACCESSION BC092292
VERSION HT.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS
Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Krausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Hsieh, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettaman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 1700)

NIH MGC Project

Direct Submission

Submitted (01-APR-2005) National Institutes of Health, Mammalian

Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgi.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mcg@hgrl.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Teague, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 193 Row: n Column: 8
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, GenomeScan gene prediction, Similarity but not identity
 to protein
 This clone has the following problem: frame shifted.

FEATURES

```

source
1..1700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech 11"
/db_xref="taxon:10090"
/clone="IMAGE:5068840"
/tissue_type="Mammary tumor metastatized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clone) outgrowth infected with the virus MMTV."
/clone_lib="NCI CGAP_Lu29"
/lab_host="DH10B"
/notes="vector: pcMV-SPORT6"

```

ORIGIN

```

Query Match      100.0%; Score 660; DB 4; Length 1700;
Best Local Similarity 100.0%; Pred. No. 3.9e-185;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGACGAGCAAAATCTATGTGACCATCATGATGCTCCCGCAGCACAGAGACTTCATCAAA 60
Db 253 GAGACGAGCAAAATCTATGTGACCATCATGATGCTCCCGCAGCACAGAGACTTCATCAAA 312
Qy 61 AACATGATTACAGGCACATCCAGCGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 313 AACATGATTACAGGCACATCCAGCGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
Qy 121 GGTGAATTTGAAGCTGGTATCTCCAGAAACGGGCGAGACCCGCGAGCATGCTCTCTGGCT 180
Db 373 GGTGAATTTGAAGCTGGTATCTCCAGAAACGGGCGAGACCCGCGAGCATGCTCTCTGGCT 432
Qy 181 TACACCTGGGTGGAACAGCTGATTGTTGGTGTCAACAAAATGGATTTCCACCGAGCCA 240
Db 433 TACACCTGGGTGGAACAGCTGATTGTTGGTGTCAACAAAATGGATTTCCACCGAGCCA 492
Qy 241 CCATACAGTCAGAGAGATACGAGAAATCGTTAAGGAAGTCAGCAGCTACATTAAGAAA 300
Db 493 CCATACAGTCAGAGAGATACGAGAAATCGTTAAGGAAGTCAGCAGCTACATTAAGAAA 552
Qy 301 ATTGGCTACACCCCTGCACAGTAGTACATTTGTGCCAATTTCTGTTGGAATGGTGACAAC 360
Db 553 ATTGGCTACACCCCTGCACAGTAGTACATTTGTGCCAATTTCTGTTGGAATGGTGACAAC 612
Qy 361 ATGCTGAGGCCAAGTCTATATGCTTGTTCGTTCAAGGGATGGAAGTCACCCGCAAGAT 420
Db 613 ATGCTGAGGCCAAGTCTATATGCTTGTTCGTTCAAGGGATGGAAGTCACCCGCAAGAT 672

```

```

Qy 421 GGCAGTGCAGTGGCACCACCGCTGCTGGAGCTTTGGATTGTATCTTACCACCAACTCGT 480
Db 673 GGCAGTGCAGTGGCACCACCGCTGCTGGAGCTTTGGATTGTATCTTACCACCAACTCGT 732
Qy 481 CCAACTGACAAAGCCTCTGGACATGCCCTCCAGGATGTCTATAAAATTTGGAGGCAATGGC 540
Db 733 CCAACTGACAAAGCCTCTGGACATGCCCTCCAGGATGTCTATAAAATTTGGAGGCAATGGC 792
Qy 541 ACTGTCCCTGTGGCCGAGTGGAGATCGTGTCTCAAACTGGCATGGTGTACCTTT 600
Db 793 ACTGTCCCTGTGGCCGAGTGGAGATCGTGTCTCAAACTGGCATGGTGTACCTTT 852
Qy 601 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCACCATGAAGCTTTGAGT 660
Db 853 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCACCATGAAGCTTTGAGT 912

```

RESULT 2

```

BM945443
LOCUS
DEFINITION
UI-M-EM0-bvh-1-15-0-UI.r1 NIH_BMAP_EM0 Mus musculus CDNA clone
IMAGE:5692190 5', mRNA sequence.
BM945443
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 673)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

```

FEATURES

```

source
1..673
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5692190"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EM0"
/notes="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCAGCAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 799.947 Seconds
(without alignments)
6831.225 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccagcaataactatgt.....tgccatgaagctttgagt 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	660	9	US-10-785-981-1
2	660	100.0	660	9	US-10-789-723-1
3	660	100.0	660	9	US-10-786-052-1
4	657.4	99.6	1040	7	US-10-424-599-16011
5	655.2	99.3	1722	6	US-10-316-253-208
6	581.6	88.1	1246	3	US-09-864-761-19622
7	581.6	88.1	1494	8	US-10-416-330-11
8	581.6	88.1	1506	7	US-10-641-643-1278
9	581.6	88.1	1636	6	US-10-374-979-74
10	581.6	88.1	1696	7	US-10-182-936A-74
11	581.6	88.1	1696	8	US-10-477-238A-653
12	581.6	88.1	1696	8	US-10-680-287A-653
13	581.6	88.1	1696	9	US-10-477-173-653
14	581.6	88.1	1720	8	US-10-278-698-242
15	581.6	88.1	1720	8	US-10-278-698-756
16	581.6	88.1	1833	7	US-10-231-956A-76
17	581.6	88.1	1833	8	US-10-684-422-254
18	581.6	88.1	1833	9	US-10-489-740-65
19	581.6	88.1	1833	9	US-10-956-157-623
20	581.6	88.1	1837	7	US-10-439-703-75
21	581.6	88.1	1950	3	US-09-864-761-2840
22	581.6	88.1	3415	3	US-09-823-245A-438
23	578.4	87.6	959	9	US-10-617-316-38

24 573.6 86.9 2106 8 US-10-684-422-60 Sequence 60, Appl
25 573.6 86.9 2106 9 US-10-367-057-166 Sequence 166, App
26 573.6 86.9 2106 9 US-10-956-157-624 Sequence 624, App
27 570.4 86.4 2128 9 US-10-955-119-22 Sequence 22, Appl
28 569.6 86.3 1709 3 US-09-822-830A-407 Sequence 407, App
29 568.4 86.1 1785 8 US-10-425-115-130623 Sequence 130623,
30 558.4 84.6 1793 9 US-10-450-763-11307 Sequence 11307, A
31 550 83.3 1309 8 US-10-425-115-130618 Sequence 130618, A
32 545.4 82.6 730 7 US-10-242-535A-45065 Sequence 45065, A
33 545.4 82.6 730 7 US-10-085-783A-45065 Sequence 45065, A
34 523 79.2 630 7 US-10-242-535A-38724 Sequence 38724, A
35 523 79.2 630 7 US-10-085-783A-38724 Sequence 38724, A
36 501.8 76.0 1982 3 US-09-864-761-3935 Sequence 3935, Ap
37 493.2 74.7 787 6 US-10-264-049-2149 Sequence 2149, Ap
38 479.4 72.6 1413 9 US-10-450-763-27989 Sequence 27989, A
39 477.6 72.4 1931 9 US-10-450-763-11410 Sequence 11410, A
40 467 70.8 1389 9 US-10-450-763-11409 Sequence 11409, A
41 467 70.8 1389 9 US-10-450-763-26843 Sequence 19051, A
42 467 70.8 1389 9 US-10-450-763-26843 Sequence 26843, A
43 458.4 69.5 546 3 US-09-871-161-466 Sequence 466, App
44 458.4 69.5 1753 7 US-10-403-571-127 Sequence 127, App
45 439.2 66.5 567 8 US-10-723-860-4749 Sequence 4749, Ap

ALIGNMENTS

RESULT 1

US-10-785-981-1

; Sequence 1, Application US/10785981

; Publication No. US20050112597A1

; GENERAL INFORMATION:

; APPLICANT: GYEONGSANGNAM-DO

; APPLICANT: Chulwook, KIM

; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE

; FILE REFERENCE: 3884-0120P

; CURRENT FILING DATE: 2004-06-26

; PRIOR APPLICATION NUMBER: KR 2003-83653

; PRIOR FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 660

; TYPE: DNA

; ORGANISM: Kagoshima Berkshire

; US-10-785-981-1

Query Match 100.0%; Score 660; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 5e-208;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGACAGCAAAATACATATGTGACCATCATTTGATGCCAGGACACAGAGACTTCATCAAA 60
Db 1 GAGACAGCAAAATACATATGTGACCATCATTTGATGCCAGGACACAGAGACTTCATCAAA 60
QY 61 AACATCATTTACAGGACATCCAGGCTGACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AACATCATTTACAGGACATCCAGGCTGACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 GGTGAATTTGAAGCTGGTATCTCTCAAGAACGGGACAGCCGCGAGCATGCTCTTCTGGCT 180
Db 121 GGTGAATTTGAAGCTGGTATCTCTCAAGAACGGGACAGCCGCGAGCATGCTCTTCTGGCT 180
QY 181 TACACCTCGGTGTGAAAACAGCTGATTTGTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
Db 181 TACACCTCGGTGTGAAAACAGCTGATTTGTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
QY 241 CCATACAGTCAGNAGATACGAGGAATCGTTAAGNAGTCAGACCTACATTAGAAA 300
Db 241 CCATACAGTCAGNAGATACGAGGAATCGTTAAGNAGTCAGACCTACATTAGAAA 300

Qy 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Db |||||
Qy 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Db |||||
Qy 361 ATGCTGGAGCAAGTGTCTAATATGCTTGGTTTCAAGGGATGGAAGTCAACCCGCAAGAT 420
Db |||||
Qy 361 ATGCTGGAGCAAGTGTCTAATATGCTTGGTTTCAAGGGATGGAAGTCAACCCGCAAGAT 420
Db |||||
Qy 421 GGAGTGCAGTGAGCCACGCTGCTGGAAAGCTTTTGGATTTGATCTTACACCACTCGT 480
Db |||||
Qy 421 GGAGTGCAGTGAGCCACGCTGCTGGAAAGCTTTTGGATTTGATCTTACACCACTCGT 480
Db |||||
Qy 481 CCAACTGACAAGCTCTGCGACTGCCCTCCAGATGCTCTATAAAATTGGAGGCAATGGC 540
Db |||||
Qy 481 CCAACTGACAAGCTCTGCGACTGCCCTCCAGATGCTCTATAAAATTGGAGGCAATGGC 540
Db |||||
Qy 541 ACTGTCCCTGTGGCCGAGTGGAGACTGGTGTCTCAAACTGGCATGGTGGTTTACCTTT 600
Db |||||
Qy 541 ACTGTCCCTGTGGCCGAGTGGAGACTGGTGTCTCAAACTGGCATGGTGGTTTACCTTT 600
Db |||||
Qy 601 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCAACCAATGAAGCTTTGAGT 660
Db |||||
Qy 601 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCAACCAATGAAGCTTTGAGT 660
Db |||||

RESULT 2
US-10-789-723-1
; Sequence 1, Application US/10789723
; Publication No. US20050112602A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: cDNA chip for screening specific genes and analyzing their
; FILE REFERENCE: function in swine
; CURRENT APPLICATION NUMBER: YLOP040109US
; CURRENT FILING DATE: US/10789,723
; PRIOR APPLICATION NUMBER: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-789-723-1

Query Match 100.0%; Score 660; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 5e-208;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGACCAAGCAAACTACTATGTGACCATCATTTGATGCCCGGAGACACAGAGACTTCATCAAA 60
Db |||||
Qy 1 GAGACCAAGCAAACTACTATGTGACCATCATTTGATGCCCGGAGACACAGAGACTTCATCAAA 60
Db |||||
Qy 61 AACATGATTACAGGCACATCCAGGCTGACTGTCTGCTCTGATTTGCTGCTGGTGT 120
Db |||||
Qy 61 AACATGATTACAGGCACATCCAGGCTGACTGTCTGCTCTGATTTGCTGCTGGTGT 120
Db |||||
Qy 121 GGTGAATTTGAAGCTGGTATCTCAAGAACGGGAGACCCGCGAGCATGCTCTTCTGGCT 180
Db |||||
Qy 121 GGTGAATTTGAAGCTGGTATCTCAAGAACGGGAGACCCGCGAGCATGCTCTTCTGGCT 180
Db |||||
Qy 181 TACACCTGGGTGTGAACAGCTGATTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
Db |||||
Qy 181 TACACCTGGGTGTGAACAGCTGATTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
Db |||||
Qy 241 CCATACAGTCAAGAGATACGAGAAATCGTTAAGGAAGTCAAGCACTCATTAAGAA 300
Db |||||
Qy 241 CCATACAGTCAAGAGATACGAGAAATCGTTAAGGAAGTCAAGCACTCATTAAGAA 300
Db |||||
Qy 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Db |||||

Db 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Qy 361 ATGCTGGAGCAAGTGTCTAATATGCTTGGTTTCAAGGGATGGAAGTCAACCCGCAAGAT 420
Db |||||
Qy 361 ATGCTGGAGCAAGTGTCTAATATGCTTGGTTTCAAGGGATGGAAGTCAACCCGCAAGAT 420
Db |||||
Qy 421 GGAGTGCAGTGAGCCACGCTGCTGGAAAGCTTTTGGATTTGATCTTACACCACTCGT 480
Db |||||
Qy 421 GGAGTGCAGTGAGCCACGCTGCTGGAAAGCTTTTGGATTTGATCTTACACCACTCGT 480
Db |||||
Qy 481 CCAACTGACAAGCTCTGCGACTGCCCTCCAGATGCTCTATAAAATTGGAGGCAATGGC 540
Db |||||
Qy 481 CCAACTGACAAGCTCTGCGACTGCCCTCCAGATGCTCTATAAAATTGGAGGCAATGGC 540
Db |||||
Qy 541 ACTGTCCCTGTGGCCGAGTGGAGACTGGTGTCTCAAACTGGCATGGTGGTTTACCTTT 600
Db |||||
Qy 541 ACTGTCCCTGTGGCCGAGTGGAGACTGGTGTCTCAAACTGGCATGGTGGTTTACCTTT 600
Db |||||
Qy 601 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCAACCAATGAAGCTTTGAGT 660
Db |||||
Qy 601 GCTCCAGTCAATGTAACTGAAGTCAAGTCTGTTGAAATGCAACCAATGAAGCTTTGAGT 660
Db |||||

RESULT 3
US-10-786-052-1
; Sequence 1, Application US/10786052
; Publication No. US20050113568A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
; FILE REFERENCE: 3884-0119P
; CURRENT APPLICATION NUMBER: US/10786,052
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: KR 2003-83652
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-786-052-1

Query Match 100.0%; Score 660; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 5e-208;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGACCAAGCAAACTACTATGTGACCATCATTTGATGCCCGGAGACACAGAGACTTCATCAAA 60
Db |||||
Qy 1 GAGACCAAGCAAACTACTATGTGACCATCATTTGATGCCCGGAGACACAGAGACTTCATCAAA 60
Db |||||
Qy 61 AACATGATTACAGGCACATCCAGGCTGACTGTCTGCTCTGATTTGCTGCTGGTGT 120
Db |||||
Qy 61 AACATGATTACAGGCACATCCAGGCTGACTGTCTGCTCTGATTTGCTGCTGGTGT 120
Db |||||
Qy 121 GGTGAATTTGAAGCTGGTATCTCAAGAACGGGAGACCCGCGAGCATGCTCTTCTGGCT 180
Db |||||
Qy 121 GGTGAATTTGAAGCTGGTATCTCAAGAACGGGAGACCCGCGAGCATGCTCTTCTGGCT 180
Db |||||
Qy 181 TACACCTGGGTGTGAACAGCTGATTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
Db |||||
Qy 181 TACACCTGGGTGTGAACAGCTGATTTGGTGTCAACAAAATGGATTCACCGAGCCA 240
Db |||||
Qy 241 CCATACAGTCAAGAGATACGAGAAATCGTTAAGGAAGTCAAGCACTCATTAAGAA 300
Db |||||
Qy 241 CCATACAGTCAAGAGATACGAGAAATCGTTAAGGAAGTCAAGCACTCATTAAGAA 300
Db |||||
Qy 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Db |||||
Qy 301 ATTGGCTACAACTGACAGTAGCATTTGTGCCAAATTTCTGGTTGGAATGTTGACAAC 360
Db |||||
Qy 361 ATGCTGGAGCAAGTGTCTAATATGCTTGGTTTCAAGGGATGGAAGTCAACCCGCAAGAT 420

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

mis Page Blank (uspto)



GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 504.283 Seconds
(without alignments)
2778.314 Million cell updates/sec

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccagcaatactatgt.....tgccaccatgaagcttttgaagt 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New.*
1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1.*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581.6	88.1	1389	8	US-10-821-234-696
2	581.6	88.1	1837	8	US-10-947-249-133
3	581.6	88.1	1837	12	US-11-000-688-278
4	577.6	87.5	1804	12	US-11-136-527-118
5	570.4	86.4	2128	8	US-10-928-033-22
6	420.6	63.7	1748	12	US-11-124-367A-101
7	420.6	63.7	1798	12	US-11-124-367A-100
8	420.6	63.7	2595	12	US-11-124-367A-99
9	411	62.3	1370	6	US-09-925-065A-28610
10	411	62.3	1370	6	US-09-925-065A-552754
11	401.4	60.8	599	6	US-09-925-065A-346940
12	387.4	58.7	2656	12	US-11-102-026A-6
13	334	50.6	918	12	US-11-102-026A-51
14	328	49.7	199130	8	US-10-995-561-13233
15	313.8	47.5	1733	12	US-11-128-061-280
16	313.8	47.5	1733	12	US-11-128-049-280
17	292.8	44.4	606	6	US-09-925-065A-369576
18	289.2	43.8	1601	12	US-11-010-239-64
19	275.2	41.7	552	6	US-09-925-065A-865515
20	254	38.5	965	8	US-10-750-185-30341

ALIGNMENTS

RESULT 1

US-10-821-234-696
; Sequence 696, Application US/10821234
; Publication No. US20050255114A1

; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia

; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0

; SEQ ID NO 696
; LENGTH: 1389

; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-821-234-696

Query Match 88.1%; Score 581.6; DB 8; Length 1389;
Best Local Similarity 92.6%; Pred. No. 8.1e-166;
Matches 611; Conservative

Mismatches 0; Indels 0; Gaps 0;

QY	1	GAGACAGCAAACTACTATGTGACCATCTGATGCCCCAGGACACAGAGACTTCATCAAA	60
DB	241	GAGACAGCAAACTACTATGTGACCATCTGATGCCCCAGGACACAGAGACTTCATCAAA	300
QY	61	AACATGATTACAGGCACATCCAGGCTGACTGTGCTGTCTCTGATTGTTGCTGTGGTGT	120
DB	301	AACATGATTACAGGCACATCTCAGGCTGACTGTGCTGTCTCTGATTGTTGCTGTGGTGT	360
QY	121	GGTGAATTTGAAGCTGGTATCTCCAAAGACGGGACACGCCGAGCATGTCTTCTGGCT	180
DB	361	GGTGAATTTGAAGCTGGTATCTCCAAAGATGGGACACGCCGAGCATGTCTTCTGGCT	420
QY	181	TACACCTGGTGTGAACAGCTGATTGTGGTGTCAACAAATGGATTCACCGAGCCA	240
DB	421	TACACCTGGTGTGAACAACTAATTTGCGGTGTTAAACAAATGGATTCACCGAGCCA	480

241	Qy	CCATACAGTCAGAGAGAGATACAGAGAAATCGTTTAAGGAAGTCAGCACCTTACATTAAGAAA	300
481	Db	CCCTACAGCCAGAGAGATATCAGGAAATCTGTTAAGGAAGTCAGCACCTTACATTAAGAAA	540
301	Qy	ATTGGCTACAACCCCTGACACAGTAGCATTTCTGTCGCCAATCTTCTGTTGGAAATGCTGACAAC	360
541	Db	ATTGGCTACAACCCCGACACAGTAGCATTTCTGTCGCCAATCTTCTGTTGGAAATGCTGACAAC	600
361	Qy	ATGCTGGAGCCAAGTGCTAAATATGTCCTTGGTTCAAGGGATGGAAAGTCACCCCAAGAT	420
601	Db	ATGCTGGAGCCAAGTGCTAAATGTCCTTGGTTCAAGGGATGGAAAGTCACCCCTAAGGAT	660
421	Qy	GGAGTGCCAGTGGGACACACGCTGCTGGAAAGCTTTGGATGTATCTTACCAACCAACTCGT	480
661	Db	GGCAATGCCAGTGGAAACACGCTGCTTGGAGCTCTGGACTGCATCTTACCACCAACTCGT	720
481	Qy	CCAACTGACAAGCCCTCTGGGACTGCGCCCTCCAGAGTCTCTATAAAATTTGGAGGCATGGC	540
721	Db	CCAACTGACAAGCCCTTGGCGCTGCGCTCTCCAGAGTGTCTACAAAATTTGGTGGTATTTGT	780
541	Qy	ACTGTCCCTGTGGCGCGAGTGAGAGACTGGTGTCTTCAAACTGGCATGGTGGTTTACTCTTT	600
781	Db	ACTGTTCTGTTGGCGGAGTGAGAGACTGGTGTCTTCAAACTGGCATGGTGGTGTCTT	840
601	Qy	GTCTCCAGTCAATGTAAACAACTGAAGTCAAGTCTGTGAAATGCAACCAATGAAGCTTTGAGT	660
841	Db	GTCTCCAGTCAAGTTTACAAAGGAGTAAATCTGTGCAATGCAACCAATGAAGCTTTGAGT	900

RESULT 2

```

US-10-947-249-133
; Sequence 133, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
; APPLICANT: Takeshi GOTO
; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-133

```

Qy	181	TACACCTCGGGTGTGAACAAGACTGATTTGTTGGTGTCAACAAAATGGATTTCCACCGAGCCA	240
Db	483	TACACACTGGGTGTGGAACAACACTAAATTTGTCGGGTGTTAACAAAATGGATTTCCACTGAGCCA	542
Qy	241	CCATACAGTCAGAGAAGAGATACGAGGAAATCGTTAAAGGAAGTCAGCACTACATTTAAGAAA	300
Db	543	CCCTACAGCCAGAAGAGATATGAGGAATTTGTTAAGGNAAGTCAGCACTTACATTTAAGAAA	602
Qy	301	ATTGGCTACAAACCGCTGACACAGTAGCAATTTGTGCAATTTCTGGTTGGAAATGGTGACAAC	360
Db	603	ATTGGCTACAAACCCGACACAGTAGCAATTTGTGCAATTTCTGGTTGGAAATGGTGACAAC	662
Qy	361	ATGCTGAGGCCAAGTCGCTAATATGCGCTTGCTCAAGGGATGGAAAGTCACCCGCCAAAGAT	420
Db	663	ATGCTGAGGCCAAGTCGCTAATATGCGCTTGCTCAAGGGATGGAAAGTCACCCGCTAAGAT	722
Qy	421	GGCAGTGCCAGTGGCACACGCGCTGCTGGAAAGCTTTTGGATTTGATCTTACCACCAACTCGT	480
Db	723	GGCAATGCCAGTGGAAACCAACGCTGCTTGAGGCTCTGGACTGCATCTTACCACCAACTCGT	782
Qy	481	CCAACTGACAAGCCCTCTGGGCACTGCCCTCCAGGATGTCATATAAAATTTGAGGCAATTGGC	540
Db	783	CCAACTGACAAGCCCTTGGCGCTTCCGCTCTCCAGGATGTCACAAAATTTGGTGGTATTGGT	842
Qy	541	ACTGTCCCTGTGGGCCGAGTGGAGACTGGTGTTCTCAAACCTGSCATGGTGGTTACCTTTT	600
Db	843	ACTGTTCTGTGTGGCCGAGTGGAGACTGGTGTTCTCAAACCCGGTATGGTGGTCAACCTTT	902
Qy	601	GCTCCAGTCAATGTAAACAAGTCAAGTCAAGTCTGCTGTGGAAATGCACCAATGAAGCTTTGAGT	660
Db	903	GCTCCAGTCAACGGTTTAAACCGGAAGTAAATCTGTGAAATGCACCAATGAAGCTTTGAGT	962

RESIT,T 3

```

RES001.3
US-11-000-688-278
; Sequence 278, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1837)
; OTHER INFORMATION: eukaryotic translation elongation factor 1
; OTHER INFORMATION: alpha 1(EEF1A1) gene.
US-11-000-688-278

```

	Query Match	88.1%	Score 581.6;	DB 12;	Length 1837;
	Best Local Similarity	92.6%;	Pred. No. 9.1e-166;		
	Matches 611;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;
Qy	1	GAGACCGCAAATACTATGTGACCATCATTTGATGCCCCAGGACACACAGACTTTCATCAA	60		
Db	303	GAGACCGCAAGTACTATGTGACTATCATTTGATGCCCCAGGACACACAGACTTTTATCAA	362		
Qy	61	AACATGATTCAGCGCAATCCAGGCTGACTGTCTCTCTGATTTGTCGCTGGTGTT	120		
Db	363	AACATGATTCAGCGCAATCTCAGGCTGACTGTCTGTCTCTGATTTGTCGCTGGTGTT	422		

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 / Search time 3206.16 Seconds
(without alignments)
9396.598 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgacggagaatc.....tagtgccattgaaatcctgg 530

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	100.0	5929	4 AB025261	- AB025261 Sus scrofa
2	526.8	99.4	5866	4 AB025262	--AB025262 Sus scrofa
3	482	90.9	5987	4 AB059399	AB059399 Bos taurus
4	477.2	90.0	5982	4 AB088366	AB088366 Equus caballus
5	470.8	88.8	1953	8 BC022376	BC022376 Homo sapiens
6	470.8	88.8	5925	6 CS018093	CS018093 Sequence
7	470.8	88.8	5925	6 CS025608	CS025608 Sequence
8	470.8	88.8	5925	6 CS119311	CS119311 Sequence
9	470.8	88.8	5925	8 AF111785	AF111785 Homo sapiens
10	470.8	88.8	5926	6 CQ731010	CQ731010 Sequence
11	459.6	86.7	5988	4 OC032574	U32574 Oryctolagus
12	450	84.9	5932	4 AB025260	AB025260 Sus scrofa
13	431.2	81.4	4910	9 AK220548	AK220548 Mus musculus
14	424.4	80.1	1806	5 CR523587	CR523587 Gallus gallus
15	424.4	80.1	5904	6 CQ733076	CQ733076 Sequence
16	424.4	80.1	6016	6 CS018091	CS018091 Sequence
17	424.4	80.1	6016	6 CS025606	CS025606 Sequence
18	424.4	80.1	6016	8 AF111783	AF111783 Homo sapiens

19	424.4	80.1	31111	5 CHRMVHE	J02714 Chicken emb
20	421.6	79.5	6010	8 HSMYOSIN	Z38133 H.sapiens m
21	421.6	79.5	6016	6 CS071067	CS071067 Sequence
22	421.6	79.5	6016	8 HUMMYOHP	M36769 Homo sapien
23	421.6	79.5	6018	6 CQ731011	CQ731011 Sequence
24	421.2	79.5	5595	9 BC008538	BC008538 Mus muscu
25	421.2	79.5	5965	4 AB059398	AB059398 Bos tauru
26	419.6	79.2	5951	5 AB021180	AB021180 Gallus ga
27	416.4	78.6	2409	8 BC093082	BC093082 Homo sapi
28	416.4	78.6	5956	6 CS018089	CS018089 Sequence
29	416.4	78.6	5956	8 AF111784	AF111784 Homo sapi
30	416.4	78.6	5957	6 CQ729334	CQ729334 Sequence
31	416.4	78.6	6085	6 CS025604	CS025604 Sequence
32	413.2	78.0	6010	5 AF272034	AF272034 Gallus ga
33	410	77.4	6031	5 AY116217	AY116217 Gallus ga
34	408.8	77.1	5980	4 AB088365	AB088365 Equus cab
35	406.8	76.8	5874	5 GGU87231	GU87231 Gallus gall
36	403.6	76.2	6022	5 AY116218	AY116218 Gallus ga
37	395.6	74.6	6067	5 AF272033	AF272033 Gallus ga
38	366.8	69.2	2520	5 AF240689	AF240689 Rana pipi
39	365.2	68.9	2520	5 AF240690	AF240690 Rana pipi
40	362.4	68.4	6032	6 AX770500	AX770500 Sequence
41	362.4	68.4	6032	8 HSMYHC	X13988 Human mRNA
42	357.2	67.4	633	9 AF336977	AF336977 Mus muscu
43	354	66.8	3333	5 BC044194	BC044194 Danio rer
44	352.4	66.5	5913	5 AY921650	AY921650 Danio rer
45	348.6	65.8	6005	5 BC076678	BC076678 Xenopus t

ALIGNMENTS

RESULT 1
AB025261
LOCUS AB025261 5929 bp mRNA linear MAM 26-JAN-2001
DEFINITION Sus scrofa mRNA for myosin heavy chain 2b, complete cds.
ACCESSION AB025261
VERSION AB025261.1 GI:5360747
KEYWORDS myosin heavy chain 2b.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (sites)
AUTHORS Chikuni,K., Tanabe,R., Muroya,S. and Nakajima,I.
TITLE Differences in molecular structure among the porcine myosin heavy chain-2a, -2x, and -2b isoforms
JOURNAL Meat Sci 57, 311-317 (2001)
REFERENCE 2 (bases 1 to 5929)
AUTHORS Chikuni,K.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1999) Koichi Chikuni, National Institute of Animal Industry, Meat Science Laboratory; Nourin-kenkyu-danchi,P.O.Box 5, Tsukuba, Ibaraki 305-0901, Japan (E-mail:chikuni@naii.affrc.go.jp, Tel:81-298-38-8686, Fax:81-298-38-8606)

FEATURES

source Location/Qualifiers
1..5929
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="Landrace"
/db_xref="taxon:9823"
/sex="male"
/tissue_type="skeletal muscle"
/dev_stage="adult"
54..5867
/codon_start=1
/product="myosin heavy chain 2b"
/protein_id="BAA82145.1"
/db_xref="GI:5360748"
/translation="MSSDQEMAIFGEAAPYLKSEKERIEAQNKPFDAKTSVFVAEPK
ESFVKGTQSGREGKVTYKTEAGATLTVKEDQVFPNPPKFDKIEDAMMTHLEPAV

CDS

LYNLKERYAAMMIYTYSGLFCVTVPNPKWLPVYNAEVVTVAYRGKQAEAPPHIFESID
NAVQMLTDRENOSILITGSGAGKTVNTKRVIOYFATIAVTEGKKEBEPTCKMOQT
LEQDILISANPLIEAFGNKTVRNDNSRGCKFIRIHFGTTGKLASDIETVLEKSRV
TFQLKABERSHIIFYQIMNSKKPELIELMLITTPDYAFVFSQSEITVPSIDDOEELMA
TDSAIETLIGTSDERSVSIYKLTGAVMHYGNLKFQKQREQAEPDGTGEVADKAAIYQ
LNSADLLKALCYPRVKGNEFVTGQTVQVYNAVAGALAKAVYDKMFLMWVTRINQOL
DTKQPOYFIVGLDIAGFIFDFNSLEQCLINFTEKLIQOFPNHHMFVLEQEEKKGG
IEWEFDGMDLAACTELIEKPMGIFSILEECCMFPKATDTSFNKLYEOLHKGKSNF
QKPKPAKGAEAHPSLIHYAGTVDNITGHLKDNKOPINETVVLGYOKSVKTLAPL
AERQSEEGTGKGGKGGSGFTVSALFRENKLMNLRSTHPSVRCIIPNETKT
PGAMEHELVLHQRCNGVLEGIRICRGKGFPSRILYADFQORYKVIVNASAIPEGOFIDS
KXASEKLLGSDIDHTQYKFGHTKVFVKGQTVQVYNAVAGALAKAVYDKMFLMWVTRINQOL
MYRVEFRKQMERRESIFICIQYNIRAFNMVHPWPKLYFKIKPLKSAETEKEMANNKE
EPEKTKEDLAKSAKRELKEMVMOEKNDLQLOVQAEADGLADAEBCDOLIKTK
IOLEAKTKEVTERADEEENAEILTAKKRELDECSLKKDIDDLLETLAKVEKHEA
TENKVNLTBEMAGLDENIAKLTKEKALQAEHQOITLDLQAEEDKNVTLTKAKTKLE
QOVDDEGLSEGLKQKRLMDLERAKRELKGLKLAQESTMDIENDKQDLDEKLLKGF
MSNLQKIDEDQALAMQOKKIKELQARTEELEBEETEAERASRAKAEKORSDLRSLE
EISERLEAGCATSAQTEMMKREAEFQKMRDLLEATLQHEATAALRKHADSVAE
LGSDIDNLRQVKOKLEKSELKMEIDDLASNMETVSKAKGNLEKMCRTLEDOLSEVK
TKSEEHORLINELSAOKARLOTESGEPSEQLDEKALVSQLSGKAFTQOIEBELKQ
LEBETKKSALAHVQSRHDCDLLREQYEEBEQAEBALQRAMSKANSEVAQWRTKYE
TDATQRTPELEEAQKALQRLQDAEBHEAVNAKCAASLEKTKQRLQNEVEDLMDVER
SNAACALDKQNFNDKILAEWKHYEETOAELEASQKESRSTELFKVKNAYBESL
DOLETTLKRNKNLQOESLDLQTEAGGKHIELEKVKQIEQKSELQALAEABEAS
LEHEEGKILRIQLELNOVKSEIDRKTAEDKEEIDOMKRNHIRVVESQMOTLDIAEIRSR
NDALRIKKMEGDLNEMEIQLNHNARQATEAIRNLNTQGVLDKOTLDLDAIRGDD
LKQGLAVERRANLQABIEELRASLEQTERSRRVAEQELLDASERVOLLHNTQNTSLI
NTRKKLETDISQIQEGMEDIVQEARNAEAKKAITDAAMAEELKEQDTSAHLERM
KXMEQTVLQHLRDLAEQALKGKKQIQKLEARVRELENEVEQKRNKAVGL
RKHERRVKELTYOTEEDRKVNLRLQDLVDLQSKVAYKQAEBAEQSNVLSKFRK
LQHELEBAERADIAESQVKNLRVKSSEVHTKVISE"

ORIGIN

Query Match 100.0%; Score 530; DB 4; Length 5929;
Best Local Similarity 100.0%; Pred. No. 1.7e-135;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCTGACTGATCGGAGATCAGTCTATCTTAATCACCGGAGATCCGGGCGAGAAAGC	60
Db	551	GCTGACTGATCGGAGATCAGTCTATCTTAATCACCGGAGATCCGGGCGAGAAAGC	610
Qy	61	TGTGAAACGAGAGCGTGTCCAGTACTTGTGCAACATCGCGCTCACTGGGAGAGAA	120
Db	611	TGTGAAACGAGAGCGTGTCCAGTACTTGTGCAACATCGCGCTCACTGGGAGAGAA	670
Qy	121	GAAGAGGAAACCTACTCTGTGCAAAATGAGGGAGCTCTGGAAGATCAGATCATCATGC	180
Db	671	GAAGAGGAAACCTACTCTGTGCAAAATGAGGGAGCTCTGGAAGATCAGATCATCATGC	730
Qy	181	CAACCCCTGCTCGAGGCTTGGCAAGCGGCAAGCGGTGAGGACGACACTCTCTCG	240
Db	731	CAACCCCTGCTCGAGGCTTGGCAAGCGGCAAGCGGTGAGGACGACACTCTCTCG	790
Qy	241	CTTTGGTAAATTCATCAGGATCCACTTCGTTACCACTGGGAAGCTGCGCTTCTGCTGACAT	300
Db	791	CTTTGGTAAATTCATCAGGATCCACTTCGTTACCACTGGGAAGCTGCGCTTCTGCTGACAT	850
Qy	301	CGAAACATATCTCTAGAGAGCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA	360
Db	851	CGAAACATATCTCTAGAGAGCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA	910
Qy	361	CCACATTTTTTATCAGATCATGTCTAACAGAACCCAGAGCTCATTTGAATGCTCCTGAT	420
Db	911	CCACATTTTTTATCAGATCATGTCTAACAGAACCCAGAGCTCATTTGAATGCTCCTGAT	970
Qy	421	CACCACCAACCATATGACTAGCTTCTGTCAGTCAAGGGAGAGTCACTGTCCCAGCAT	480
Db	971	CACCACCAACCATATGACTAGCTTCTGTCAGTCAAGGGAGAGTCACTGTCCCAGCAT	1030
Qy	481	TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCCATTGAAATCTCTGG	530
Db	1031	TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCCATTGAAATCTCTGG	1080

RESULT 2	AB025262	AB025262	5866 bp	mrna	linear	MAM 26-JAN-2001
LOCUS	Sus scrofa	mrna for myosin heavy chain 2x, complete cds.				
DEFINITION	AB025262					
ACCESSION	AB025262					
VERSION	AB025262.1	GI:5360749				
KEYWORDS	myosin heavy chain 2x.					
SOURCE	Sus scrofa (pig)					
ORGANISM	Sus scrofa					
REFERENCE	1 (sites)					
AUTHORS	Chikuni K., Tanabe R., Muroya S. and Nakajima I.					
TITLE	Differences in molecular structure among the porcine myosin heavy chain-2a, -2x, and -2b isoforms					
JOURNAL	Meat Sci 57, 311-317 (2001)					
REFERENCE	2 (bases 1 to 5866)					
AUTHORS	Chikuni K.					
TITLE	Direct Submission					
JOURNAL	Submitted (23-WAR-1999) Koichi Chikuni, National Institute of Animal Industry, Meat Science Laboratory; Nourin-kenkyu-danchi, P.O. box 5, Tsukuba, Ibaraki 305-0901, Japan (E-mail:chikuni@niai.affrc.go.jp, Tel:81-298-38-8686, Fax:81-298-38-8606)					
FEATURES	Location/Qualifiers					
source	1. .5866					
	/organism="Sus scrofa"					
	/mol_type="mrna"					
	/strain="Landrace"					
	/db_xref="taxon:9823"					
	/sex="male"					
	/tissue_type="skeletal muscle"					
	/dev_stage="adult"					
	42. .5861					
	/codon_start=1					
	/product="myosin heavy chain 2x"					
	/protein_id="BAA82146.1"					
	/db_xref="GI:5360750"					
	/translation="MSSDQEMAIFGEAAPLYRKSEKRIEIQNKPFDAKTSVFVAEPK ESVFTQVSGGGKTVTKTEAGATLVKEDQVPMNPPFKFIDEMAMMTHLHEPAP LYNLKERYAAMMIYTYSGLFCVTVPNPKWLPVYNAEVVTVAYRGKQAEAPPHIFESID NAVQMLTDRENOSILITGSGAGKTVNTKRVIOYFATIAVTEGKKEBEPTCKMOQT LEQDILISANPLIEAFGNKTVRNDNSRGCKFIRIHFGTTGKLASDIETVLEKSRV TFQLKABERSHIIFYQIMNSKKPELIELMLITTPDYAFVFSQSEITVPSIDDOEELMA TDSAIETLIGTSDERSVSIYKLTGAVMHYGNLKFQKQREQAEPDGTGEVADKAAIYQ LNSADLLKALCYPRVKGNEFVTGQTVQVYNAVAGALAKAVYDKMFLMWVTRINQOL DTKQPOYFIVGLDIAGFIFDFNSLEQCLINFTEKLIQOFPNHHMFVLEQEEKKGG IEWEFDGMDLAACTELIEKPMGIFSILEECCMFPKATDTSFNKLYEOLHKGKSNF QKPKPAKGAEAHPSLIHYAGTVDNITGHLKDNKOPINETVVLGYOKSVKTLAPL TGAAGDAEAGGKGGKGGSGFTVSALFRENKLMNLRSTHPSVRCIIPNET KTGAMHEHELVLHQRCNGVLEGIRICRGKGFPSRILYADFQORYKVIVNASAIPEGOFIDS KXASEKLLGSDIDHTQYKFGHTKVFVKGQTVQVYNAVAGALAKAVYDKMFLMWVTRINQOL MYRVEFRKQMERRESIFICIQYNIRAFNMVHPWPKLYFKIKPLKSAETEKEMANNKE EPEKTKEDLAKSAKRELKEMVMOEKNDLQLOVQAEADGLADAEBCDOLIKTK IOLEAKTKEVTERADEEENAEILTAKKRELDECSLKKDIDDLLETLAKVEKHEA TENKVNLTBEMAGLDENIAKLTKEKALQAEHQOITLDLQAEEDKNVTLTKAKTKLE QOVDDEGLSEGLKQKRLMDLERAKRELKGLKLAQESTMDIENDKQDLDEKLLKGF MSNLQKIDEDQALAMQOKKIKELQARTEELEBEETEAERASRAKAEKORSDLRSLE EISERLEAGCATSAQTEMMKREAEFQKMRDLLEATLQHEATAALRKHADSVAE LGSDIDNLRQVKOKLEKSELKMEIDDLASNMETVSKAKGNLEKMCRTLEDOLSEVK TKSEEHORLINELSAOKARLOTESGEPSEQLDEKALVSQLSGKAFTQOIEBELKQ LEBETKKSALAHVQSRHDCDLLREQYEEBEQAEBALQRAMSKANSEVAQWRTKYE TDATQRTPELEEAQKALQRLQDAEBHEAVNAKCAASLEKTKQRLQNEVEDLMDVER SNAACALDKQNFNDKILAEWKHYEETOAELEASQKESRSTELFKVKNAYBESL DOLETTLKRNKNLQOESLDLQTEAGGKHIELEKVKQIEQKSELQALAEABEAS LEHEEGKILRIQLELNOVKSEIDRKTAEDKEEIDOMKRNHIRVVESQMOTLDIAEIRSR NDALRIKKMEGDLNEMEIQLNHNARQATEAIRNLNTQGVLDKOTLDLDAIRGDD LKQGLAVERRANLQABIEELRASLEQTERSRRVAEQELLDASERVOLLHNTQNTSLI NTRKKLETDISQIQEGMEDIVQEARNAEAKKAITDAAMAEELKEQDTSAHLERM KXMEQTVLQHLRDLAEQALKGKKQIQKLEARVRELENEVEQKRNKAVGL RKHERRVKELTYOTEEDRKVNLRLQDLVDLQSKVAYKQAEBAEQSNVLSKFRK LQHELEBAERADIAESQVKNLRVKSSEVHTKVISE"					

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 449.779 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgacgggagaatc.....tagtgccattgaaatcctgg 530

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	100.0	530	14	ADZ89039 Pig growt
2	530	100.0	530	14	ADZ79332 Swine gro
3	530	100.0	530	14	ADZ77169 Pig growt
4	470.8	88.8	5925	10	ADZ29577 Human tum
5	470.8	88.8	5925	10	ADW95930 DNA enco
6	470.8	88.8	5925	14	ADX15796 DNA enco
7	470.8	88.8	5925	14	ADX25983 Novel cel
8	432.4	81.6	5874	5	AAS85420 DNA enco
9	424.4	80.1	6016	14	ADW95928 cDNA enco
10	424.4	80.1	6016	14	ADX15794 DNA enco
11	424.4	80.1	6016	14	ADX25985 Novel cel
12	421.6	79.5	6010	12	ADQ22038 Human sof
13	421.6	79.5	6010	12	ADQ22007 Human sof
14	421.6	79.5	6010	12	ADQ17241 Human sof
15	421.6	79.5	6010	12	ADQ17288 Human sof
16	421.6	79.5	6016	4	AAS7390 Human sof
17	421.2	79.5	5595	14	ADX26120 Novel cel
18	416.4	78.6	5956	14	ADW95926 cDNA enco
19	416.4	78.6	6085	14	ADX15792 DNA enco

20	362.4	68.4	6032	8	ACA89885	Aca89885 Gene diff
21	352.8	66.6	6035	14	ADX26230	Adx26230 Novel cel
22	347.6	65.6	5992	13	ADQ80266	Adq80266 Skeletal
23	328.4	62.0	2477	14	AEB50291	Aeb50291 Human myo
24	328.4	62.0	5395	14	AEB50288	Aeb50288 Human myo
25	328.4	62.0	5661	2	AAV21518	Aav21518 Rattus no
26	328.4	62.0	5930	10	ADB52833	Adb52833 Primary r
27	328.4	62.0	5930	13	ADV41112	Adv41112 Rat cardi
28	328.4	62.0	5930	14	ADX26221	Adx26221 Novel cel
29	328.4	62.0	6057	14	AEB50285	Aeb50285 Human myo
30	328.4	62.0	6177	14	AEB50286	Aeb50286 Human myo
31	328.4	62.0	6290	14	AEB50284	Aeb50284 Human myo
32	328.4	62.0	6903	14	AEB50292	Aeb50292 Human myo
33	328.4	62.0	8921	14	AEB50283	Aeb50283 Human myo
34	328.4	62.0	9119	14	AEB50287	Aeb50287 Human myo
35	320.4	60.5	5886	13	ADS97707	Ads97707 Rabbit al
36	320.4	60.5	12801	13	ADS97709	Ads97709 Rabbit al
37	319.2	60.2	6054	14	ADX26110	Adx26110 Novel cel
38	313.2	59.1	5918	11	ACN92725	Acn92725 Breast ca
39	308	58.1	4775	10	ADK18363	Adk18363 Human NOV
40	308	58.1	5780	10	ADK18365	Adk18365 Human NOV
41	308	58.1	6008	10	ADK18367	Adk18367 Human NOV
42	308	58.1	6008	12	ADP13461	Adp13461 Renal cel
43	308	58.1	6008	14	ADX25975	Adx25975 Novel cel
44	301.6	56.9	5925	12	ADP72935	Adp72935 Renal tox
45	301.6	56.9	5925	13	ADV41113	Adv41113 Rat cardi

ALIGNMENTS

RESULT 1

ADZ89039

ID ADZ89039 standard; DNA; 530 BP.

XX ADZ89039;

XX

28-JUL-2005 (first entry)

DE Pig growth factor II (GF II) gene, seq id 2.

XX Growth; biochip; swine; hog raising; growth factor II; gene; ds.

OS Sub scrofa; Kagoshima Berkshire.

XX US2005112597-A1.

XX 26-MAY-2005.

XX 26-FEB-2004; 2004US-00785981.

XX 24-NOV-2003; 2003KR-00083653.

XX (KIMC/) KIM C.

XX (YEOJ/) YEO J.

XX (LEEJ/) LEE J.

XX (SONG/) SONG Y.

XX (CHOK/) CHO K.

XX (CHUN/) CHUNG K.

XX (KIMI/) KIM I.

XX (JINS/) JIN S.

XX (PARK/) PARK S.

XX (JUNG/) JUNG J.

XX (LEEM/) LEE M.

XX (KWON/) KWON E.

XX (CHOE/) CHO E.

XX (CHOH/) CHO H.

XX (SHIN/) SHIN S.

XX (NAMEH/) NAM H.

XX (HONG/) HONG Y.

XX (HONG/) HONG S.

XX (KANG/) KANG Y.

XX (HAYY/) HA Y.

```
PA (ROUJ/) ROU J.
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX WPI: 2005-403340/41.
XX Functional cDNA chip useful for screening and function analysis of growth
XX specific genes according to breeds and tissues of swine, comprises
PT substrate and probe comprising growth specific genes in muscle and fat
PT tissues of swine.
XX
XX Claim 2; SEQ ID NO 2; 8pp; English.
XX
XX The invention relates to a functional cDNA chip (I) for screening and
XX function analysis of growth specific genes according to breeds and
XX tissues of swine, comprises a probe comprising growth specific genes in
XX muscle and fat tissues of swine, and a substrate on which the probe is
XX immobilized. Further disclosed is a kit (KI) useful for screening and
XX functional analysis of growth specific gene according to breeds and
XX tissues of swine, comprising (I) integrated in it, Cy5-dCTP or Cy3-dCTP
XX bound cDNA from RNA of the tissue to be screened, a fluorescence scanning
XX system, and a computer analysis system. (I) and (KI) are useful for
XX screening and function analysis of growth specific gene according to
XX breeds and tissues of swine. (I) is useful in the swine improvement and
XX breeding of a new breed, and in the hog raising industry. The current
XX sequence represents the pig growth factor II (GF II) gene.
XX
XX Sequence 530 BP; 154 A; 137 C; 127 G; 112 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 530; DB 14; Length 530;
Best Local Similarity 100.0%; Pred. No. 7e-159;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGACTGATCGGAGGAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGGAAGAC 60
Db 1 GCTGACTGATCGGAGGAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGGAAGAC 60
Qy 61 TGTGAACACGAGCGGTGTCATCAGTACTTTGGCCCAATCGCGTCACTGGGGAGAGAA 120
Db 61 TGTGAACACGAGCGGTGTCATCAGTACTTTGGCCCAATCGCGTCACTGGGGAGAGAA 120
Qy 121 GAAGGAGGAACCTACTCTCTGCAAAATGCAGGGGACTCTGGAAGATCAGATCATCAGTGC 180
Db 121 GAAGGAGGAACCTACTCTCTGCAAAATGCAGGGGACTCTGGAAGATCAGATCATCAGTGC 180
Qy 181 CAACCCCTGCTCAGGCGCTTTGGCAACGCGCAAGACCGTGGAGAACGACAACTCCTCTCG 240
Db 181 CAACCCCTGCTCAGGCGCTTTGGCAACGCGCAAGACCGTGGAGAACGACAACTCCTCTCG 240
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCCTACCTGGGAAGCTGCTCTGTCGACAT 300
Db 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCCTACCTGGGAAGCTGCTCTGTCGACAT 300
Qy 301 CGAAACATATCTTCTAGAGAAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGACTA 360
Db 301 CGAAACATATCTTCTAGAGAAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGACTA 360
Qy 361 CCACATTTTATCAGATCATGTCTAAACGAAGCCAGAGCTCATTTGAATGCTCTGAT 420
Db 361 CCACATTTTATCAGATCATGTCTAAACGAAGCCAGAGCTCATTTGAATGCTCTGAT 420
Qy 421 CACCACCAACCCATATCAGTACGCTTCGTCAGTCAAGGGGAGATCACTGTCCTCCAGCAT 480
Db 421 CACCACCAACCCATATCAGTACGCTTCGTCAGTCAAGGGGAGATCACTGTCCTCCAGCAT 480
Qy 481 TGATGACCAAGAGGAGCTGATGGCCACAGATAGTGCCATTGAAATCTCTGG 530
Db 481 TGATGACCAAGAGGAGCTGATGGCCACAGATAGTGCCATTGAAATCTCTGG 530
```

```
RESULT 2
ADZ79332
ID ADZ79332 standard; cDNA; 530 BP.
XX
AC ADZ79332;
XX
DT 28-JUL-2005 (first entry)
XX
DE Swine growth factor GB-II cDNA for cDNA chip diagnostic method.
XX
KW biochip; screening; EST; expressed sequence tag; probe; muscle;
KW immobilization; gene expression; polymorphism; diagnosis;
KW animal breeding; growth factor; ss.
XX
OS Unidentified.
XX
PN US2005112602-A1.
XX
PD 26-MAY-2005.
XX
PF 27-FEB-2004; 2004US-00789723.
XX
PR 24-NOV-2003; 2003KR-00083651.
XX
XX (KIMC/) KIM C.
PA (YEOJ/) YEO J.
PA (LEEJ/) LEE J.
PA (SONG/) SONG Y.
PA (CHOK/) CHO K.
PA (CHUN/) CHUNG K.
PA (KIMI/) KIM I.
PA (JINS/) JIN S.
PA (PARK/) PARK S.
PA (JUNG/) JUNG J.
PA (LEEM/) LEE M.
PA (KWON/) KWON E.
PA (CHOE/) CHO E.
PA (CHOH/) CHO H.
PA (SHIN/) SHIN S.
PA (NAMH/) NAM H.
PA (HONG/) HONG Y.
PA (KANG/) KANG Y.
PA (HAYI/) HA Y.
PA (ROUJ/) ROU J.
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX
XX WPI: 2005-371656/38.
XX
XX New cDNA chip comprising a probe capable of detecting marker genes
XX specifically expressed in the muscle and fat tissues of swine, and a
XX substrate, useful for screening and function analysis of swine genes.
XX
XX Claim 9; SEQ ID NO 2; 15pp; English.
XX
XX The invention relates to a cDNA chip for screening and function analysis
XX of swine genes comprising a probe capable of detecting marker genes
XX specifically expressed in the muscle and fat tissues of swine and a
XX substrate on which the probe is immobilized. The invention also includes
XX a kit for screening and function analysis of swine genes comprising the
XX cDNA chip. The cDNA chip is useful for screening and function analysis of
XX swine genes, particularly for comparing genetic expression according to
XX swine breeds and tissues, genetic mutation screening, genetic
XX polymorphism interpretation, development of new drugs for disease
XX treatment and disease diagnosis, swine improvement. This sequence
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3140.18 Seconds
(without alignments)
7896.735 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgacggagaatc.....tagtgccattgaatctcgg 530

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462.8	87.3	5667	11	DQ052205 Homo sapi
2	462.8	87.3	5667	11	DQ052206 Pan trogl
3	450	84.9	2674	4	AK041122 Mus muscu
4	447.6	84.5	752	8	DN423235 LIB4216-0
5	431.2	81.4	3339	4	AK029328 Mus muscu
6	429.2	81.0	623	8	DN423628 LIB4216-0
7	427.6	80.7	648	8	DN421412 LIB4216-0
8	427.6	80.7	771	8	DN425844 LIB4216-0
9	424.4	80.1	5820	11	DQ029772 Homo sapi
10	422.4	79.7	650	8	DN424241 LIB4216-1
11	421.6	79.5	5814	11	DQ052207 Homo sapi
12	418	78.9	5814	11	DQ052208 Pan trogl
13	416.4	78.6	6062	4	EX510904 Homo sapi
14	415.2	78.3	785	8	DN423007 LIB4216-0
15	412.4	77.8	675	6	CD621454 56028779J
16	398.8	75.2	710	8	DN421704 LIB4216-0
17	374.8	70.7	817	8	EX901213 JGI CAAM9
18	369	69.6	493	5	BU387960 603858632
19	368.2	69.5	5805	11	DQ029773 Pan trogl
20	367.8	69.4	539	1	AW918573 EST349877
21	367	69.2	649	8	DN421699 LIB4216-0
22	366.6	69.2	667	8	DN421346 LIB4216-0

23	364.6	68.8	659	3	BM486201	BM486201 pgmlc.pk0
24	364	68.7	763	8	DN426850	DN426850 LIB4216-0
25	362.4	68.4	5823	11	DQ036335	DQ036335 Homo sapi
26	354.4	66.9	558	7	CN698824	CN698824 E0413C04-
27	354.4	66.9	626	7	CN699265	CN699265 E0419A05-
28	351.6	66.3	591	7	CR756940	CR756940 CR756940
29	350.8	66.2	933	7	CK017852	CK017852 AGENCOURT
30	346	65.3	847	8	DN935535	DN935535 AGENCOURT
31	344.6	65.0	5823	11	DQ036336	DQ036336 Pan trogl
32	343.2	64.8	5802	11	DQ029771	DQ029771 Pan trogl
33	338.2	63.8	599	8	DN423594	DN423594 LIB4216-0
34	336.8	63.5	839	8	CX390733	CX390733 JGI_XZT38
35	336.4	63.5	5826	11	DQ051102	DQ051102 Homo sapi
36	335	63.2	442	1	AV599364	AV599364 AV599364
37	335	63.2	719	7	CK687877	CK687877 ZF101-P00
38	334.8	63.2	551	3	BM179887	BM179887 dail13a03
39	331	62.5	774	6	CF287168	CF287168 AGENCOURT
40	329.4	62.2	395	5	BU946705	BU946705 P824U-133
41	328.8	62.0	864	8	CX328746	CX328746 JGI_XZT67
42	328.4	62.0	643	8	DN376020	DN376020 LIB38529
43	324.6	61.2	818	8	CX312040	CX312040 JGI_XZT11
44	324.2	61.2	5802	11	DQ029770	DQ029770 Homo sapi
45	322	60.8	603	6	CD499600	CD499600 CDA40-C08

ALIGNMENTS

RESULT 1
DQ052205
LOCUS Homo sapiens MYH1 gene, VIRTUAL TRANSCRIPT, partial sequence, 5667 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens MYH1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ052205
VERSION DQ052205.1 GI:66905676
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5667)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) Plos Biol. 3 (6), E170 (2005)
PUBLISHED 15869325
REFERENCE 2 (bases 1 to 5667)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES
Location/Qualifiers
source 1..5667
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
gene <1..>5667
/gene="MYH1"
ORIGIN /locus_tag="HC20221"

Query Match 87.3%; Score 462.8; DB 11; Length 5667;
Best Local Similarity 92.9%; Pred. No. 1.3e-125;
Matches 485; Conservative 0; Mismatches 37; Indels 0; Gaps 0;


```
QY 9 ATCGGGAGATCAGTCTTAAATCACCGGAGATCCGGGGCAGGAAGACTGTGAACA 68
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
506 ATCGGGAGATCAGTCTTATCTGATCCCGGAGATCTGGCGCAGGAAGACTGTGAACA 565

QY 69 CGAAGCGTGTATCCAGTCTTTCACCAATCGCCGCTCACTGGGGGAGAGAAGAGG 128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
566 CCAAGCGTGTATCCAGTCTTTCACCAATTCGAGTTACTGGGGGAGAGAAGAGG 625

QY 129 AACCTACTCTCGCAAAATCGAGGGGACTCTGGAAGATCAGATCATCAGTGCCAAACCCC 188
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
626 AAGTTACTCTCGCAAAATCGAGGGGACTCTGGAAGATCAATCAATCATCAGTGCCAAACCCC 685

QY 189 TGCTCGAGGCTTTGGCAACCGCAAGCCGTGAGGACGACACTCTCTCGCTTTGGTA 248
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
686 TACTGGAGGCTTTGGCAACCGCAAGCCGTGAGGAAATGCAACTCTCTCGCTTTGGTA 745

QY 249 AATTTCATCAGATCCACTTCGGTACCACTGGGAAGCTGGCTTCTGCTGACATCGAAACAT 308
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
746 AATTTCATCAGATCCACTTCGGTACCACTGGGAAGCTGGCTTCTGCTGATATTGAAACAT 805

QY 309 ATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTTAAAGGAGGAGAAAGCTACCAATTT 368
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
806 ATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTTAAAGGCTGAAAGAGCTATCATATTT 865

QY 369 TTTATCAGATCATGTCTAAACAAGAGCCAGAGCTCAATTGAAATGCTCTGATCACCACCA 428
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
866 TTTATCAGATCATGTCTAAACAAGAGCCAGAGCTCAATTGAAATGCTCTGATCACCACCA 925

QY 429 ACCATATGACTACGCTTCTGTCAGTCAAGGGAGATCACTGTCCCGCAGCATGATGACC 488
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
926 ACCATATGACTACGCTTCTGTCAGTCAAGGGAGATCACTGTCCCGCAGCATGATGACC 985

QY 489 AAGAGGAGCTGATGGCCACAGATAGTCCCATTTGAAATCTCTGG 530
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
986 AAGAGGAGCTGATGGCCACAGATAGTCCCATTTGAAATCTCTGG 1027

RESULT 2
DQ052206 5667 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes MYH1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ052206
VERSION DQ052206.1 GI:66905677
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 5667)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 5667)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
1..5667
/mol_type="genomic DNA"
```

```
/db_xref="taxon:9598"
<1..>5667
/gene="MYH1"
/locus_tag="HC20221"

ORIGIN
Query Match 87.3%; Score 462.8; DB 11; Length 5667;
Best Local Similarity 92.9%; Pred. No. 1.3e-125;
Matches 485; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 9 ATCGGGAGATCAGTCTTAAATCACCGGAGATCCGGGGCAGGAAGACTGTGAACA 68
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
506 ATCGGGAGATCAGTCTTATCTGATCCCGGAGATCTGGCGCAGGAAGACTGTGAACA 565

QY 69 CGAAGCGTGTATCCAGTCTTTCACCAATCGCCGCTCACTGGGGGAGAGAAGAGG 128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
566 CCAAGCGTGTATCCAGTCTTTCACCAATTCGAGTTACTGGGGGAGAGAAGAGG 625

QY 129 AACCTACTCTCGCAAAATCGAGGGGACTCTGGAAGATCAGATCATCAGTGCCAAACCCC 188
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
566 AAGTTACTCTCGCAAAATCGAGGGGACTCTGGAAGATCAATCAATCATCAGTGCCAAACCCC 685

QY 189 TGCTCGAGGCTTTGGCAACCGCAAGCCGTGAGGACGACACTCTCTCGCTTTGGTA 248
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
686 TACTGGAGGCTTTGGCAACCGCAAGCCGTGAGGAAATGCAACTCTCTCGCTTTGGTA 745

QY 249 AATTTCATCAGATCCACTTCGGTACCACTGGGAAGCTGGCTTCTGCTGACATCGAAACAT 308
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
746 AATTTCATCAGATCCACTTCGGTACCACTGGGAAGCTGGCTTCTGCTGATATTGAAACAT 805

QY 309 ATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTTAAAGGAGGAGAAAGCTACCAATTT 368
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
806 ATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTTAAAGGCTGAAAGAGCTATCATATTT 865

QY 369 TTTATCAGATCATGTCTAAACAAGAGCCAGAGCTCAATTGAAATGCTCTGATCACCACCA 428
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
866 TTTATCAGATCATGTCTAAACAAGAGCCAGAGCTCAATTGAAATGCTCTGATCACCACCA 925

QY 429 ACCATATGACTACGCTTCTGTCAGTCAAGGGAGATCACTGTCCCGCAGCATGATGACC 488
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
926 ACCATATGACTACGCTTCTGTCAGTCAAGGGAGATCACTGTCCCGCAGCATGATGACC 985

QY 489 AAGAGGAGCTGATGGCCACAGATAGTCCCATTTGAAATCTCTGG 530
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
986 AAGAGGAGCTGATGGCCACAGATAGTCCCATTTGAAATCTCTGG 1027

RESULT 3
AK041122 2674 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DEFINITION enriched library, clone:A530084A17 product:TYPE 3 MTOSIN HEAVY
CHAIN homolog [Rana pipiens], full insert sequence.
ACCESSION AK041122
VERSION AK041122.1 GI:26334226
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED Genome Res. 10 (10), 1617-1630 (2000)
11042159
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 130.047 Seconds
(without alignments)
7244.353 Million cell updates/sec

Title: US-10-785-981-2
Perfect score: 530
Sequence: 1 gctgactgacgggagaatc.....tagtgccattgaaatcctgg 530

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PPTRUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.8	88.8	5925	3	US-09-949-016-5233
2	424.4	80.1	6016	3	US-09-949-016-1054
3	424.4	80.1	6016	3	US-09-949-016-2264
4	362.4	68.4	6011	3	US-09-949-016-3017
5	347.6	65.6	5992	3	US-09-949-016-546
6	347.6	65.6	5992	3	US-09-949-016-2263
7	328.4	62.0	5661	3	US-08-938-105-2
8	308	58.1	6008	3	US-09-949-016-5058
9	144	27.2	6644	3	US-08-875-435B-5
10	141.4	26.7	5919	3	US-08-875-435B-2
11	141.2	26.6	6175	3	US-08-875-435B-1
12	141	26.6	5883	3	US-09-949-016-5001
13	139.2	26.3	5574	3	US-09-917-254-40
14	139.2	26.3	6861	3	US-09-949-016-1240
15	139.2	26.3	6861	3	US-09-949-016-1241
16	139.2	26.3	6861	3	US-09-949-016-1242
17	123.8	23.4	7596	3	US-09-023-655-1463
18	122.2	23.1	7453	3	US-09-949-016-4965
19	109.4	20.6	3581	3	US-09-949-016-16975
20	105.2	19.8	28355	3	US-09-949-016-16975
21	105	19.8	4688	3	US-09-949-016-4522
22	98.2	18.5	7501	3	US-09-620-312D-249
23	94.6	17.8	30271	3	US-09-949-016-12796
24	94.6	17.8	30272	3	US-09-949-016-14006

ALIGNMENTS

RESULT 1

US-09-949-016-5233
; Sequence 5233, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5233
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5233

Query Match	88.8%	Score	470.8	DB	3	Length	5925
Best Local Similarity	93.0%	Pred. No.	7.3e-140				
Matches	493	Conservative	0	Mismatches	37	Indels	0
Gaps	0						

QY 1 GCTGACTGATCGGAGAAATCAGTCTATCTTAATCACCGGAGAAATCGGGGAGGAGAAC 60
DB 498 GCTGACTGATCGGAGAAATCAGTCTATCTTATCACCGGAGAAATCGGGGAGGAGAAC 557
QY 61 TGTGAACACGAAAGCGTGTATCAGTCTTGTGCAATCGCGTCACTGGGGAGAGAA 120
DB 558 TGTGAACACGAAAGCGTGTATCAGTCTTGTGCAATCGCGTCACTGGGGAGAGAA 617
QY 121 GAGGAGGAGAACTTACTCTTGGCAAAATGAGGGGAGTCTTGGAGATCAGATCATCATGTC 180
DB 618 GAGGAGGAGAACTTACTCTTGGCAAAATGAGGGGAGTCTTGGAGATCAGATCATCATGTC 677
QY 181 CAACCCCTGCTCGAGGCTTTTGGCAACGCGCAAGACCGTGAGGAGAGCAAACTCTCTCG 240
DB 678 CAACCCCTGCTCGAGGCTTTTGGCAACGCGCAAGACCGTGAGGAGAGCAAACTCTCTCG 737
QY 241 CTTTGTGTAATTCATCAGGATCCACTTCGGTACCACTGGGAACTGGCTTCTGCTGACAT 300

```
Db      738 CTTTGGTAAATTTCATCAGGATCCATTCGGTACCAACAGGGAAGCTGCTTCTGCTGATAT 797
Qy      301 CGAAACATATCTTCTAGAGAAGTCTAGAGTCACTTTCCAGCTAAAGCGCAGAAAGAGCTTA 360
Db      798 TGAACACATATCTTCTGAGAAGTCTAGAGTACTTTCCAGCTAAAGGCTGAAAGAGCTA 857
Qy      361 CCACATTTTATCAGATCATGTCTTCAACAGAGCCAGAGCTCATTTGAATGCTCCCTGAT 420
Db      858 TCATATTTTATCAGATCATGTCTTCAACAGAGCCAGAGTCTAATTTGAATGCTCCCTGAT 917
Qy      421 CACCACCAACCCATATGACTACGCTTCCTGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db      918 CACCACCAACCCATACGATTATGCTTCCTGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 977
Qy      481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGGCAATTGAAATCCTGG 530
Db      978 TGATGACCAAGAGAGTGTGATGGCTGACAGATAGTGGCAATTGAAATCCTGG 1027

RESULT 2
US-09-949-016-1054
; Sequence 1054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1054
; LENGTH: 6016
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1054

Query Match      80.1%; Score 424.4; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125;
Matches 464; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy      1 GCTGACTGATCGGAGAAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGGAAGAC 60
Db      609 GCTAACTGATCGTGAAGAACCAAGTCAATCTTGATTACTGGAGAAATCTGGTCAGGGAAGAC 668
Qy      61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCGCAAAATCGCGCTCACTGGGGAAGAA 120
Db      669 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCGCAAAATCGCGCTCACTGGGGAAGAA 728
Qy      121 GAAGGAGAACCTTACTCTGGCAAAATCGAGGAGCTCTGGAAGATCAGATCATCATGTC 180
Db      729 AAAAGAGGAACCTGCTCTGGCAAAATCGAGGAGCTCTGGAAGATCAAAATCATCATGTC 788
Qy      181 CAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 240
Db      789 TAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 848
Qy      241 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 300
Db      849 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 908
Qy      181 CAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 240
Db      789 TAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 848
Qy      241 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 300
Db      849 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 908
Qy      301 CGAAACATATCTTCTAGAGAAGTCTAGAGTCACTTTCCAGCTAAAGCGCAGAAAGAGCTTA 360
Db      909 TGAACACATATCTGCTAGAGAAGTCCCGAGTACTTTTCAGCTAAAGGCTGAAAGAGCTA 968
Qy      361 CCACATTTTATCAGATCATGTCTTCAACAGAGCCAGAGCTCATTTGAATGCTCCCTGAT 420
```

```
Db      969 CCACATTTTATCAATCTCTCCATAGAAACAGAGCTCATTTGAATGCTTCTGAT 1028
Qy      421 CACCACCAACCCATATGACTACGCTTCCTGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db      1029 CACCACCAACCCATATGACTTCGCAATTTGTAGCAAGGGGAAATTTACTGTGCCAGCAT 1088
Qy      481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGGCAATTGAAATCCTGG 530
Db      1089 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGGCTGTGGACATCCTCG 1138

RESULT 3
US-09-949-016-2264
; Sequence 2264, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2264
; LENGTH: 6016
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2264

Query Match      80.1%; Score 424.4; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125;
Matches 464; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy      1 GCTGACTGATCGGAGAAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGGAAGAC 60
Db      609 GCTAACTGATCGTGAAGAACCAAGTCAATCTTGATTACTGGAGAAATCTGGTCAGGGAAGAC 668
Qy      61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCGCAAAATCGCGCTCACTGGGGAAGAA 120
Db      669 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCGCAAAATCGCGCTCACTGGGGAAGAA 728
Qy      121 GAAGGAGAACCTTACTCTGGCAAAATCGAGGAGCTCTGGAAGATCAGATCATCATGTC 180
Db      729 AAAAGAGGAACCTGCTCTGGCAAAATCGAGGAGCTCTGGAAGATCAAAATCATCATGTC 788
Qy      181 CAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 240
Db      789 TAACCCCTCTCTGAGGCTTTGCGCAACCGCAAGACCGTGGAGAACGACAACCTCTCTCG 848
Qy      241 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 300
Db      849 CTTTGGTAAATTCATCAGGATCCACTTCGTTACCAATCGCGTCACTGGGAGCTGCTCTGAT 908
Qy      301 CGAAACATATCTTCTAGAGAAGTCTAGAGTCACTTTCCAGCTAAAGCGCAGAAAGAGCTTA 360
Db      909 TGAACACATATCTGCTAGAGAAGTCCCGAGTACTTTTCAGCTAAAGGCTGAAAGAGCTA 968
Qy      361 CCACATTTTATCAGATCATGTCTTCAACAGAGCCAGAGCTCATTTGAATGCTCCCTGAT 420
Db      969 CCACATTTTATCAATCTCTGCTCAATAGAAACAGAGCTCATTTGAATGCTTCTGAT 1028
Qy      421 CACCACCAACCCATATGACTACGCTTCCTGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db      1029 CACCACCAACCCATATGACTTCGCAATTTGTAGCAAGGGGAAATTTACTGTGCCAGCAT 1088
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 641.579 Seconds
(without alignments)
6831.225 Million cell updates/sec

Title: US-10-785-981-2
Perfect score: 530
Sequence: 1 gctgactgacggagaatc.....tagtgcattgaaatcctgg 530

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	530	100.0	530	9	US-10-785-981-2
2	530	100.0	530	9	US-10-789-723-2
3	530	100.0	530	9	US-10-786-052-2
4	470.8	88.8	5925	8	US-10-335-053-26
5	432.4	81.6	5874	9	US-10-450-763-21224
6	421.6	79.5	6010	8	US-10-723-860-57
7	421.6	79.5	6010	8	US-10-723-860-105
8	421.6	79.5	6010	8	US-10-723-860-4827
9	421.6	79.5	6010	8	US-10-723-860-4858
10	416.4	78.6	5956	9	US-10-783-271-100
11	362.4	68.4	6523	6	US-10-062-674-1980
12	320.4	60.5	5886	8	US-10-798-037-5
13	320.4	60.5	12801	8	US-10-798-037-5
14	313.2	59.1	5918	7	US-10-198-846-13875
15	308	58.1	4775	7	US-10-336-472-17
16	308	58.1	5780	7	US-10-336-472-19
17	308	58.1	6008	7	US-10-336-472-21
18	308	58.1	6008	7	US-10-717-597-197
19	301.6	56.9	5925	7	US-10-191-803-104
20	248.8	46.9	6149	7	US-10-188-186-95
21	244.2	46.1	716	6	US-10-257-826A-65
22	227.2	42.9	6237	9	US-10-450-763-12161
23	222.4	42.0	6968	10	US-11-097-143-40166

24	162.8	30.7	6915	7	US-10-188-186-47	Sequence 47, Appl
25	143.2	27.0	5896	6	US-10-085-198-131	Sequence 131, App
26	141	26.6	5883	9	US-10-956-157-859	Sequence 859, App
27	141	26.6	6354	5	US-10-084-817-158	Sequence 158, App
28	141	26.6	7274	9	US-10-696-909A-48	Sequence 48, Appl
29	141	26.6	7396	6	US-10-028-248A-35	Sequence 35, Appl
30	141	26.6	7396	7	US-10-107-782-35	Sequence 35, Appl
31	139.2	26.3	2486	8	US-10-357-930-22131	Sequence 22131, A
32	139.2	26.3	2486	8	US-10-357-930-27993	Sequence 27993, A
33	139.2	26.3	2535	3	US-09-927-597-13	Sequence 13, Appl
34	139.2	26.3	2535	7	US-10-486-057-13	Sequence 13, Appl
35	139.2	26.3	6655	7	US-10-296-115-526	Sequence 526, App
36	139.2	26.3	6861	5	US-10-171-311-161	Sequence 161, App
37	139.2	26.3	6861	6	US-10-341-434-102	Sequence 102, App
38	139.2	26.3	6861	9	US-10-923-035-18	Sequence 18, Appl
39	139.2	26.3	6900	5	US-10-171-311-163	Sequence 163, App
40	139.2	26.3	6900	7	US-10-764-425-13	Sequence 13, Appl
41	139.2	26.3	11085	5	US-10-116-802-14	Sequence 14, Appl
42	136.6	25.8	2097	3	US-09-927-597-5	Sequence 5, Appl
43	136.6	25.8	2097	9	US-10-486-057-5	Sequence 5, Appl
44	136.6	25.8	2316	3	US-09-927-597-7	Sequence 7, Appl
45	136.6	25.8	2316	9	US-10-486-057-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-785-981-2
; Sequence 2, Application US/10785981
; Publication No. US20050112597A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
; FILE REFERENCE: 3884-0120P
; CURRENT FILING DATE: 2004-06-26
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-785-981-2

Query Match	100.0%	Score 530;	DB 9;	Length 530;
Best Local Similarity	100.0%	Pred. No. 7.6e-170;		
Matches 530;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	GCTGACTGATCGGAGAAATCAGTCTTATTAATCAGCGGAGAAATCGGGGAGGAAAGAC	60	
Db	1	GCTGACTGATCGGAGAAATCAGTCTTATTAATCAGCGGAGAAATCGGGGAGGAAAGAC	60	
Qy	61	TGTGAACGAGACGGTGTATCCAGTACTTTGCCAATCCCGTCACTCGGGGAGAGAA	120	
Db	61	TGTGAACGAGACGGTGTATCCAGTACTTTGCCAATCCCGTCACTCGGGGAGAGAA	120	
Qy	121	GAAGGAGGAAACCTTACTCTCGGCAAAATGCGGGGACTCTGGAAGATCAGATCATCATGTC	180	
Db	121	GAAGGAGGAAACCTTACTCTCGGCAAAATGCGGGGACTCTGGAAGATCAGATCATCATGTC	180	
Qy	181	CAACCCCTGCTCGAGGCTTTGGGCAACGCGCAAGACCGTGAGGAAACGACAACTCTCTCG	240	
Db	181	CAACCCCTGCTCGAGGCTTTGGGCAACGCGCAAGACCGTGAGGAAACGACAACTCTCTCG	240	
Qy	241	CTTTGGTAAATTCATCAGATCCACTTCGGTACCACTGGGAAGCTGCTTCTGCTGACAT	300	
Db	241	CTTTGGTAAATTCATCAGATCCACTTCGGTACCACTGGGAAGCTGCTTCTGCTGACAT	300	

```
Qy 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Db 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Qy 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Db 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Qy 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Qy 481 TGATGACCAAGAGGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530
Db 481 TGATGACCAAGAGGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530

RESULT 2
US-10-789-723-2
; Sequence 2, Application US/10789723
; Publication No. US20050112602A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: cDNA chip for screening specific genes and analyzing their
; TITLE OF INVENTION: function in swine
; FILE REFERENCE: YLOP040109US
; CURRENT APPLICATION NUMBER: US/10/789,723
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: KR 2003-83651
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-789-723-2

Query Match 100.0%; Score 530; DB 9; Length 530;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGACTGATCGGAGATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGAAAGAC 60
Db 1 GCTGACTGATCGGAGATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGAAAGAC 60
Qy 61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCCACAATCCCGTCACTGGGAGAAAGAA 120
Db 61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCCACAATCCCGTCACTGGGAGAAAGAA 120
Qy 121 GAAGAGGAACTTCTCTCGCAAAATGACGGGAGCTCTGGAAGATCAGATCATCAGTGC 180
Db 121 GAAGAGGAACTTCTCTCGCAAAATGACGGGAGCTCTGGAAGATCAGATCATCAGTGC 180
Qy 181 CAACCCCTGCTCGAGGCTTTGGCAAGCGCAAGACCGTGAAGACGACAACTCTCTCG 240
Db 181 CAACCCCTGCTCGAGGCTTTGGCAAGCGCAAGACCGTGAAGACGACAACTCTCTCG 240
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACTGGGAAAGCTGCTGCTGACAT 300
Db 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACTGGGAAAGCTGCTGCTGACAT 300
Qy 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Db 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Qy 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Db 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Qy 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480

RESULT 4
US-10-335-053-26
; Sequence 26, Application US/10335053
; Publication No. US20040241653A1
```

```
Db 421 CACCACCAACCATATGACTAGCTTACGCTTTCGTAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Qy 481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530
Db 481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530

RESULT 3
US-10-786-052-2
; Sequence 2, Application US/10786052
; Publication No. US20050113568A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
; FILE REFERENCE: 3884-0119P
; CURRENT APPLICATION NUMBER: US/10/786,052
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: KR 2003-83652
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-786-052-2

Query Match 100.0%; Score 530; DB 9; Length 530;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGACTGATCGGAGAAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGAAAGAC 60
Db 1 GCTGACTGATCGGAGAAATCAGTCTATCTTAATCACCGGAGAAATCCGGGGCAGAAAGAC 60
Qy 61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCCACAATCCCGTCACTGGGAGAAAGAA 120
Db 61 TGTGAACACGAAGCGTGTCTATCCAGTACTTTGCCACAATCCCGTCACTGGGAGAAAGAA 120
Qy 121 GAAGAGGAACTTCTCTCGCAAAATGACGGGAGCTCTGGAAGATCAGATCATCAGTGC 180
Db 121 GAAGAGGAACTTCTCTCGCAAAATGACGGGAGCTCTGGAAGATCAGATCATCAGTGC 180
Qy 181 CAACCCCTGCTCGAGGCTTTGGCAAGCGCAAGACCGTGAAGACGACAACTCTCTCG 240
Db 181 CAACCCCTGCTCGAGGCTTTGGCAAGCGCAAGACCGTGAAGACGACAACTCTCTCG 240
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACTGGGAAAGCTGCTGCTGACAT 300
Db 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACTGGGAAAGCTGCTGCTGACAT 300
Qy 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Db 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGCGAGAAAGCTA 360
Qy 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Db 361 CCACATTTTATCAGATCATGTCTAAACAAGACCGCAGAGCTCAATTGAAATGCTCTGAT 420
Qy 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Db 421 CACCACCAACCATATGACTAGCGCTTCGTCAGTCAAGGGGAGATCACTGTCCCCAGCAT 480
Qy 481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530
Db 481 TGATGACCAAGAGAGCTGATGGCCACAGATAGTGCATTTGAAATCTCTGG 530

RESULT 4
US-10-335-053-26
; Sequence 26, Application US/10335053
; Publication No. US20040241653A1
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 404.955 Seconds
(without alignments)
2778.314 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgacgggagatc.....tagtgccattgaaatcctgg 530

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New.*
1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470.8	88.8	5925	12	US-11-000-688-1358
2	416.4	78.6	6062	12	US-11-150-888-13
3	352.8	66.6	6035	12	US-11-136-527-3751
4	328.4	62.0	6021	12	US-11-136-527-274
5	303.6	57.3	5941	12	US-11-136-527-275
6	146	27.5	6060	12	US-11-136-527-2285
7	145.6	27.5	6377	12	US-11-069-834-57
8	145.2	27.4	7355	12	US-11-069-834-47
9	144.8	27.3	6442	12	US-11-069-834-55
10	144.2	27.2	6786	12	US-11-069-834-59
11	141	26.6	7474	12	US-11-069-834-49
12	139.2	26.3	6900	12	US-11-000-688-1142
13	138.8	26.2	4239	8	US-10-995-561-148
14	138.8	26.2	6025	8	US-10-995-561-143
15	138.8	26.2	6148	8	US-10-995-561-147
16	138.8	26.2	6187	8	US-10-995-561-144
17	138.8	26.2	6886	8	US-10-995-561-149
18	138.8	26.2	6925	8	US-10-995-561-145
19	138	26.0	6185	8	US-10-995-561-146
20	135	25.5	2097	12	US-11-136-527-3099

21	130.2	24.6	7666	12	US-11-069-834-51	Sequence 51, Appl
22	126.6	23.9	7653	12	US-11-136-527-2934	Sequence 2934, Ap
23	123.8	23.4	255	8	US-10-909-125-1961	Sequence 1961, Ap
24	122.2	23.1	7619	12	US-11-069-834-53	Sequence 53, Appl
25	109.6	20.7	2529	12	US-11-136-527-3182	Sequence 3182, Ap
26	108.6	20.5	4652	12	US-11-136-527-3350	Sequence 3350, Ap
27	86.6	16.3	5347	9	US-11-072-512-1310	Sequence 1310, Ap
28	85	16.0	7336	12	US-11-136-527-2202	Sequence 2202, Ap
29	84.4	15.9	1568	8	US-10-750-185-37934	Sequence 37934, A
30	84.4	15.9	1568	8	US-10-750-623-37934	Sequence 37934, A
31	83.8	15.8	4456	12	US-11-136-527-318	Sequence 318, App
32	79	14.9	5649	12	US-11-136-527-2615	Sequence 863384,
33	78.8	14.9	636	6	US-09-525-065A-863384	Sequence 863384,
34	78.6	14.8	2727	9	US-11-072-512-1480	Sequence 1480, Ap
35	78	14.7	201	8	US-10-995-561-4989	Sequence 4989, Ap
36	78	14.7	201	8	US-10-995-561-5016	Sequence 5016, Ap
37	78	14.7	201	8	US-10-995-561-5043	Sequence 5043, Ap
38	78	14.7	201	8	US-10-995-561-5073	Sequence 5073, Ap
39	78	14.7	201	8	US-10-995-561-5100	Sequence 5100, Ap
40	78	14.7	201	8	US-10-995-561-5125	Sequence 5125, Ap
41	78	14.7	201	8	US-10-995-561-5144	Sequence 5144, A
42	76.6	14.5	1141	8	US-10-750-185-49953	Sequence 49953, A
43	76.6	14.5	1141	8	US-10-750-623-49953	Sequence 49953, A
44	68.8	13.0	538	6	US-09-525-065A-951135	Sequence 951135,
45	68.8	13.0	548	6	US-09-525-065A-944582	Sequence 944582,

ALIGNMENTS

RESULT 1

US-11-000-688-1358
; Sequence 1358, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; CURRENT FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1358
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5925)
; OTHER INFORMATION: myosin, heavy polypeptide 1, skeletal
; OTHER INFORMATION: muscle, adult (MvH1) gene.
US-11-000-688-1358

Query Match	88.8%	Score	470.8	DB	12	Length	5925
Best Local Similarity	93.0%	Pred. No.	7.2e-127				
Matches	493	Conservative	0	Mismatches	37	Indels	0
QY	1	GCTGACTGATCGGAGAAATCAGTCTATCTTATACCGGAGAAATCGGGGACGAGAAC	60				
Db	498	GCTGACTGATCGGAGAAATCAGTCTATCTTATACCGGAGAAATCGGGGACGAGAAC	557				
QY	61	TGTGAACAGAAAGCGTGTCTATCTTATACCGGAGAAATCGGGGACGAGAAC	120				
Db	558	TGTGAACAGAAAGCGTGTCTATCTTATACCGGAGAAATCGGGGACGAGAAC	617				
QY	121	GAAGGAGGAACCTACTCTCTGGGAAATCAGGGGACTCTGGAGATCATCATCATGTC	180				

```
Db 618 GAAGGAGAAAGTTACTTCTGCAAAATGACGGGACTCTCGAAGATCAAAATCATCACTGC 677
Qy 181 CAACCCCTGCTGAGGCTTTGGCAACGCCAGACCGGTGAGGAAACGACAACTCTCTCG 240
Db 678 CAACCCCTACTGAGGCTTTGGCAACGCCAGACCGGTGAGGAAATGACAACTCTCTCG 737
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACCTGGGAAGCTGGCTTCTGCTGACAT 300
Db 738 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACAGGGAATCGCTTCTGCTGATAT 797
Qy 301 CGAAACATATCTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGACAGAAAGAGCTA 360
Db 798 TGAACATACTCTGAGAGTCTAGAGTCTCTTCCAGCTAAAGGCTGAAGAGCTA 857
Qy 361 CCACATTTTATCAGATCATGTCTAAACAGAGCCAGAGCTCATTTGAAATGCTCTGAT 420
Db 858 TCATATTTTATCAGATCATGTCTAAACAGAGCCAGATCTAAATGAAATGCTCTGAT 917
Qy 421 CACCACCAACCCATACACTACGCTTCGTCACTCAAGGGAGATCACTGTCCCCAGCAT 480
Db 918 CACCACCAACCCATACACTATGCTTCGTCACTCAAGGGAGATCACTGTCCCCAGCAT 977
Qy 481 TGATGACCAAGAGAGTGTGATGCGCACAGATAGTGCATTTGAAATCCTGG 530
Db 978 TGATGACCAAGAGAGTGTGATGCGTACAGATAGTGCATTTGAAATCCTGG 1027

RESULT 2
US-11-150-888-13
; Sequence 13, Application US/11150888
; Publication No. US20060003959A1
; GENERAL INFORMATION:
; APPLICANT: Burden, Steven
; APPLICANT: Littman, Daniel
; TITLE OF INVENTION: Methods and Agents for Maintaining
; TITLE OF INVENTION: Muscle Mass and for Preventing Muscle Atrophy and Biomarkers
; TITLE OF INVENTION: For Monitoring Same
; FILE REFERENCE: 1049-1-048N
; CURRENT FILING DATE: 2005-06-10
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 6062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-150-888-13

Query Match 78.6%; Score 416.4; DB 12; Length 6062;
Best Local Similarity 86.6%; Pred. No. 5.1e-111;
Matches 459; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 1 GCTCACTGATCGGAGATCAGTCTATCTTAAATCAACCGGAGAAATCCGGGCGAGAAAGAC 60
Db 589 GCTCACTGACCGAGAGATCAGTCAATCCTGATCACTGAGAAATCTGGTCAAGGAAAGAC 648
Qy 61 TGTGAACACGAAGCGTGTCACTCACTTAAATCAACCGGAGAAATCCGGGCGAGAAAGAA 120
Db 649 TGTGAACACGAAGCGTGTCACTCACTTAAATCAACCGGAGAAATCTGGTCAAGGAAAGAA 708
Qy 121 GAAGGAGAAACCTACTCTGCAAAATGCGGGGACTCTGGAAGATCAGATCATCACTGTC 180
Db 709 GAAGGAGAAATTAATCTGCAAAATACAGGGGACTCTGGAAGATCAATCATCACTGTC 768
Qy 181 CAACCCCTGCTCGAGGCTTTGGCAACGCCAGACCGGTGAGGAAACCACTCTCTCG 240
Db 769 CAACCCCTACTGAGGCTTTGGCAACGCCAGACCGGTGAGGAAATGACAACTCTCTCG 828
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACCTGGGAAGCTGGCTTCTGCTGACAT 300
Db 829 CTTTGGTAAATTCATCAGGATCCACTTTGGCACTACTGGAAATCGGCACTCTGCTGATAT 888
```

```
Qy 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGACAGAAAGAGCTA 360
Db 889 TGAACATATCTCTAGAGAGTCTAGAGTGTGTTTCCAGCTTAAGGCTGAGAGAAAGTTA 948
Qy 361 CCACATTTTATCAGATCATGTCTAAACAGAGCCAGAGCTCATTTGAAATGCTCTCTGAT 420
Db 949 TCATATTTTATCAGATTCATCGAATGAAGAACCCAGAACTTATTGAATGCTCTCTGAT 1008
Qy 421 CACCACCAACCCATATGATACCGCTTCGTCACTCAAGGGAGATCACTGTCCCCAGCAT 480
Db 1009 TACCACGAACCCATATGATTAACCAATTTGTCACTCAAGGGAGATCACTGTGGCCAGCAT 1068
Qy 481 TGATGACCAAGAGAGTGTGATGCGCACAGATAGTGCATTTGAAATCCTGG 530
Db 1069 CGATGATCAGGAAGAACTGATGCGCACAGATAGTGTATTGATATTTTGG 1118

RESULT 3
US-11-136-527-3751
; Sequence 3751, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3751
; LENGTH: 6035
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3751

Query Match 66.6%; Score 352.8; DB 12; Length 6035;
Best Local Similarity 80.6%; Pred. No. 1.7e-92;
Matches 427; Conservative 0; Mismatches 97; Indels 6; Gaps 1;

Qy 1 GCTGACTGATCGGAGAAATCAGTCTATCTTAAATCAACCGGAGAAATCCGGGCGAGAAAGAC 60
Db 588 GCTGACGGATCGTGAGAAACCAAGTCCATCTGATCACCGGAGAAATCCGGGCGAGAAAGAC 647
Qy 61 TGTGAACACGAAGCGTGTCACTCACTTGTGCAATCCCGTCACTGGGGAGAAAGAA 120
Db 648 GGTGAACACCAAGCGTGTCACTCACTTGTGCAATTCAGCCACTGGGACCTTGC 707
Qy 121 GAAGGAGAAACCTACTCTCTGGCAAAATGCGGGGACTCTGGAAGATCAGATCATCACTGTC 180
Db 708 CAAGAAAGAGACTC-----CAAAATGAAGGGGACCCCTGGAAGATCAAAATCATCAGCGC 761
Qy 181 CAACCCCTGCTCGAGGCTTTGGCAACGCCAGACCGGTGAGGAAACCACTCTCTCG 240
Db 762 CAACCCCTGCTCGAGGCTTTGGGAAATGCAAGCCGTGAGGAAATGACAACTCTTCCCG 821
Qy 241 CTTTGGTAAATTCATCAGGATCCACTTCGGTACCACCTGGGAAGCTGGCTTCTGCTGACAT 300
Db 822 CTTTGGCAAGTTTATCCGATCCATTTCCGCAACCACTGGGAAGCTGGCTCTGAGATAT 881
Qy 301 CGAAACATATCTTCTAGAGAGTCTAGAGTCACTTTCCAGCTAAAGGACAGAAAGAGCTA 360
Db 882 TGAACCTTATCTGCTGAAAGTCCAGAGTCACTTCCAGCTGAAGGCTGAGAGAAAGCTA 941
Qy 361 CCACATTTTATCAGATCATGTCTAAACAGAGCCAGAGCTCATTTGAAATGCTCTCTGAT 420
Db 942 TCACATCTTCTACAGATCTTTTCCAAACAGAGCCGGAATCTGATCGAGTTGCTGCTGAT 1001
Qy 421 CACCACCAACCCATATGATCACTACGCTTCGTCACTCAAGGGAGATCACTGTGCCAGCAT 480
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 3563.08 Seconds
(without alignments)
9396.598 Million cell updates/sec

Title: US-10-785-981-3
Perfect score: 589
Sequence: 1 gttgtcccttaaatatgat.....tagtgcattgaaatcctgg 589

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr:*

9: gb_ro:*

10: gb_sts:*

11: gb_sy:*

12: gb_un:*

13: gb_vl:*

14: gb_htg:*

15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	528.4	89.7	1427	6	BD079915
2	528.4	89.7	1677	6	CQ721905
3	528.4	89.7	1932	6	CQ848036
4	528.4	89.7	2357	6	AX077789
5	528.4	89.7	2448	8	AK000759
6	528.4	89.7	2703	6	AR338661
7	528.4	89.7	104089	8	AC012488
8	526.8	89.4	1932	8	AV116969
9	526.8	89.4	2392	8	BC001243
10	498	84.6	2445	8	AB169610
11	498	84.6	2474	8	AB169783
12	466	79.1	184340	14	AC155201
13	353.8	60.1	776	6	BD101385
14	353.8	60.1	776	6	BD021447
15	317.8	54.0	517	10	G57776
16	275	46.7	2266	9	BC013617
17	275	46.7	199753	9	AC153650
18	275	46.7	256751	9	AC122925

19	261.2	44.3	308652	14	AC121478
20	260	44.1	227221	14	AC096437
c 21	234.8	39.9	232244	14	AC114524
22	234.8	39.9	238999	14	AC128410
23	178	30.2	2316	5	AJ720404
24	137	23.3	336	6	AR391327
25	137	23.3	336	6	AR393032
26	137	23.3	336	6	AR489762
27	137	23.3	336	6	AR494003
28	137	23.3	336	6	AX093332
29	103	17.5	209897	14	AC134122
c 30	103	17.5	239398	14	AC105708
c 31	94.8	16.1	105208	9	AL671897
32	82.2	14.0	870	6	BD097742
33	82.2	14.0	870	6	BD017804
34	80.2	13.6	2167	5	BC051619
c 35	78.6	13.3	121251	5	AL591593
36	63.8	10.8	482	10	BV103802
c 37	55.8	9.5	197797	14	AC151536
38	50	8.5	5866	4	AB025261
39	50	8.5	5929	4	AB025261
c 40	48.8	8.3	2000	6	AX655393
41	48.2	8.2	886	6	AR526567
42	48.2	8.2	1514	6	AR510239
43	48.2	8.2	1705	6	CQ597990
44	48.2	8.2	1705	6	CQ847838
45	48.2	8.2	1799	2	AY069456

ALIGNMENTS

RESULT 1	BD079915	1427 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	Cancer-associated nucleic acids and polypeptides.				
DEFINITION	BD079915				
ACCESSION	BD079915				
VERSION	BD079915.1	GI:22625518			
KEYWORDS	JP 2001516009-A/581.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1427)				
AUTHORS	Old, L. J., Scanlan, M. J., Stockert, E., Gure, A., Chen, Y. T., Gout, I., Oghare, M., Obata, Y., Pfreundschuh, M., Tureci, O. and Sahin, U.				
TITLE	Cancer-associated nucleic acids and polypeptides				
JOURNAL	Patent: JP 2001516009-A 581 25-SEP-2001;				
COMMENT	LUDWIG INSTITUTE FOR CANCER RESEARCH				
	OS Homo sapiens (human)				
	PN JP 2001516009-A/581				
	PD 25-SEP-2001				
	PF 15-JUL-1998 JP 2000503425				
	PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599 PR				
	10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR				
	J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI TSENG				
	CHEN, IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFREUNDSCHEH, PI				
	OZLEM TURECI,				
	PI UGUR SAHIN				
	PC				
	G01N33/574, A61K38/00, A61K39/395, A61K45/00, A61K48/00, PC				
	A61P35/00,				
	PC C07K14/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/02,				
	PC C12N15/00				
	CC Cancer-associated nucleic acids and polypeptides. FH Key				
	Location/Qualifiers				
	FT source 1..1427				
	FT Location/Qualifiers				
	1..1427				
	Location/Qualifiers				
	1..1427				

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3489.74 Seconds
(without alignments)
7896.735 Million cell updates/sec

Title: US-10-785-981-3
Perfect score: 589
Sequence: 1 gttgtcccttaatatgat.....tagtgcattgaatactctgg 589

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528.4	89.7	755	2	BG031674 602300827
2	528.4	89.7	1213	4	CR621606 full-leng
3	528.4	89.7	1415	4	CR621025 full-leng
4	528.4	89.7	1512	4	CR594310 full-leng
5	528.4	89.7	1689	4	CR594492 full-leng
6	528.4	89.7	1932	11	DQ053604 Homo sapi
7	527.6	89.6	1012	1	AL560753
8	527.4	89.5	1112	3	BM802677
9	526.8	89.4	615	2	BE175655
10	526.8	89.4	908	2	BG779206
11	526.8	89.4	1035	1	AL528352
12	525.2	89.2	1932	11	DQ053605
13	525	89.1	862	2	BG166586
14	524	89.0	839	1	AL529078
15	517.6	87.9	702	2	BG678319
16	479.6	81.4	890	1	AL548432
17	478.4	81.2	882	2	BF132189
18	478	81.2	884	2	BF984476
19	440.4	74.8	485	3	BM766987
20	428.4	72.7	527	1	AW386704
21	419	71.1	604	1	AW581575
22	415	70.5	423	9	AQ206754 HS_3241_A

23	411.4	69.8	507	6	CF134508
24	400.4	68.0	457	2	BE175777
25	399.6	67.8	767	8	Z78323
26	385.6	65.5	861	8	DN520090
27	384.4	65.3	386	9	AQ207000
28	380.4	64.6	587	2	BG403231
29	361.4	61.4	984	7	CO581479
30	360	61.1	757	3	BM990680
31	357.4	60.7	444	2	BE696484
32	356.8	60.6	382	2	BE773649
33	353.4	60.0	466	2	BE773939
34	344	58.4	742	7	CO894304
35	341.8	58.0	912	2	BF213807
36	334.4	56.8	559	1	AW952425
37	328.4	55.8	812	8	DN872098
38	325.4	55.2	759	2	BG164923
39	324.4	55.1	673	2	BE887500
40	317.8	54.0	366	2	BE836524
41	317.8	54.0	517	9	AQ341682
42	315.8	53.6	470	1	AJ662831
43	314.4	53.4	716	7	CK835329
44	308.2	52.3	384	9	AQ717690
45	306.2	52.0	579	2	BE536026

ALIGNMENTS

RESULT 1
BG031674

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG031674 755 bp mRNA linear EST 24-JAN-2001
602300827F1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:4402182 5',
mRNA sequence.
BG031674.1 GI:12422197
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10110 row: f column: 07
High quality sequence stop: 717.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4402182"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: Breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match

89.7%; Score 528.4; DB 2; Length 755;

Best Local Similarity 98.7%; Pred. No. 1.1e-132; Matches 543; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GTTGTTCCTTTAAATATGATGTTGCCAACAAGCTGCATTTGGAGACTCATTCACGTAATATT 60
Db |||||
QY 40 GTTGTTCCTTTAAATATGATGTTGCCAACAAGCTGCATTTGGAGACTCATTCACGTAATATT 99
Db |||||
QY 61 TCCAATGTGCCACTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACACATGAAG 120
Db |||||
QY 100 TCCAATGTGCCACTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACACATGAAG 159
Db |||||
QY 121 GAAGTAATTCAGCAGTTCATTTGATGTTCTGAGTGTAGCAGTCAAGAAACCTGCTTGTGT 180
Db |||||
QY 160 GAAGTAATTCAGCAGTTCATTTGATGTTCTGAGTGTAGCAGTCAAGAAACCTGCTTGTGT 219
Db |||||
QY 181 TTACCTAGGATGAAACCTCGACAGCAAAATGAAGTTTGGAAACGTCGTGTAGGAAAGCA 240
Db |||||
QY 220 TTACCTAGGATGAAACCTCGACAGCAAAATGAAGTTTGGAAACGTCGTGTAGGAAAGCA 279
Db |||||
QY 241 AATGTTGCAATCTGTTTCTGGGGGCAATGATTCATGCTTATTCGAAACCTTGTCTGAC 300
Db |||||
QY 280 AATGTTGCAATCTGTTTCTGGGGGCAATGATTCATGCTTATTCGAAACCTTGTCTGAC 339
Db |||||
QY 301 CGTCATATTCCTTTAGATGAACCAATGATCTTCTTAATCTAGCTTTCATAGCTGAAGAA 360
Db |||||
QY 340 CGTCATATTCCTTTAGATGAACCAATGATCTTCTTAATCTAGCTTTCATAGCTGAAGAA 399
Db |||||
QY 361 AAGACCATGCCAATCTACCTTTAAGAGAGAGGGAATAAACAGAAATAAATGTGAATA 420
Db |||||
QY 400 AAGACCATGCCAATCTACCTTTAAGAGAGAGGGAATAAACAGAAATAAATGTGAATA 459
Db |||||
QY 421 CCTTCAGAGAAATCTCTAAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 480
Db |||||
QY 460 CCTTCAGAGAAATCTCTAAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 519
Db |||||
QY 481 -TCAGTGTACAGATCGAATCAGAGAGAGGCGGAGCTAAGGAACTACAGCTGTTAGC 539
Db |||||
QY 520 GTCAAGTACAGATCGAATCAGAGAGAGGCGGAGCTAAGGAACTACAGCTGTTAGC 579
Db |||||
QY 540 TGATGACCAA 549
Db |||||
QY 580 CCTTCCCGAA 589
Db |||||

CR621606 1213 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DD004YK21 of Neuroblastoma Cot
50-normalized of Homo sapiens (human).

CR621606
VERSION CR621606.1 GI:50502413
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1213)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source Location/Qualifiers
1..1213
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD004YK21"
/tissue_type="Neuroblastoma Cot 50-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 89.7%; Score 528.4; DB 4; Length 1213;
Best Local Similarity 98.7%; Pred. No. 1.2e-132;
Matches 543; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GTTGTTCCTTTAAATATGATGTTGCCAACAAGCTGCATTTGGAGACTCATTCACGTAATATT 60
Db |||||
QY 12 GTTGTTCCTTTAAATATGATGTTGCCAACAAGCTGCATTTGGAGACTCATTCACGTAATATT 71
Db |||||
QY 61 TCCAATGTGCCACTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACACATGAAG 120
Db |||||
QY 72 TCCAATGTGCCACTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACACATGAAG 131
Db |||||
QY 121 GAAGTAATTCAGCAGTTCATTTGATGTTCTGAGTGTAGCAGTCAAGAAACCTGCTTGTGT 180
Db |||||
QY 132 GAAGTAATTCAGCAGTTCATTTGATGTTCTGAGTGTAGCAGTCAAGAAACCTGCTTGTGT 191
Db |||||
QY 181 TTACCTAGGATGAAACCTCGACAGCAAAATGAAGTTTGGAAACGTCGTGTAGGAAAGCA 240
Db |||||
QY 192 TTACCTAGGATGAAACCTCGACAGCAAAATGAAGTTTGGAAACGTCGTGTAGGAAAGCA 251
Db |||||
QY 241 AATGTTGCAATCTGTTTCTGGGGGCAATGATTCATGCTTATTCGAAACCTTGTCTGAC 300
Db |||||
QY 252 AATGTTGCAATCTGTTTCTGGGGGCAATGATTCATGCTTATTCGAAACCTTGTCTGAC 311
Db |||||
QY 301 CGTCATATTCCTTTAGATGAACCAATGATCTTCTTAATCTAGCTTTCATAGCTGAAGAA 360
Db |||||
QY 312 CGTCATATTCCTTTAGATGAACCAATGATCTTCTTAATCTAGCTTTCATAGCTGAAGAA 371
Db |||||
QY 361 AAGACCATGCCAATCTACCTTTAAGAGAGAGGGAATAAACAGAAATAAATGTGAATA 420
Db |||||
QY 372 AAGACCATGCCAATCTACCTTTAAGAGAGAGGGAATAAACAGAAATAAATGTGAATA 431
Db |||||
QY 421 CCTTCAGAGAAATCTCTAAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 480
Db |||||
QY 432 CCTTCAGAGAAATCTCTAAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 491
Db |||||
QY 481 -TCAGTGTACAGATCGAATCAGAGAGAGGCGGAGCTAAGGAACTACAGCTGTTAGC 539
Db |||||
QY 492 GTCAAGTACAGATCGAATCAGAGAGAGGCGGAGCTAAGGAACTACAGCTGTTAGC 551
Db |||||
QY 540 TGATGACCAA 549
Db |||||
QY 580 CCTTCCCGAA 561
Db |||||

RESULT 3

CR621025

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

CR621025 1415 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DC023YH23 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).

CR621025

CR621025

HTC; CNSLT_CDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1415)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 499.848 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttccttaaatatgat.....tagtgccattgaaatcctgg 589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	589	14	Adz89040 Pig growt
2	589	100.0	589	14	Adz79333 Swine gro
3	589	100.0	589	14	Adz77170 Pig growt
4	528.4	89.7	1427	2	Aax40181 Lung canc
5	528.4	89.7	1932	13	Adq89911 Antagonis
6	528.4	89.7	2357	4	Aaf60005 Human syn
7	528.4	89.7	2414	6	Ab189966 Human pol
8	528.4	89.7	2703	4	Aai58275 Human pol
9	528.4	89.7	2703	5	Adq98482 DNA encod
10	528.4	89.7	2703	9	Adb48242 Novel hum
11	528.4	89.7	6499	4	Aak86748 Human imm
12	526.8	89.4	2451	10	Adi40392 Human pur
13	517.4	87.8	2410	4	Aai60061 Human col
14	474.8	80.6	610	14	ACL57351 Human col
15	391.6	66.5	2734	5	Aas84622 DNA encod
16	353.8	60.1	776	4	Aai97610 Human neu
17	137	23.3	396	4	Aaf94959 Human ova
18	137	23.3	396	6	Ab148909 Ovarian c
19	137	23.3	396	6	Abt03226 Human ova

20	137	23.3	396	11	ADM10819	Human ova
21	137	23.3	396	12	ADJ11149	Represent
22	137	23.3	396	12	ADM43410	Human ova
23	82.2	14.0	870	4	AAI93967	Human neu
24	59.4	10.1	492	9	ACH21529	Human adu
25	59	10.0	1208	5	AAS84621	DNA encod
26	51	8.7	469	14	ADZ89041	Pig growt
27	51	8.7	469	14	ADZ79334	Swine gro
28	51	8.7	469	14	ADZ77171	Pig growt
29	50	8.5	530	14	ADZ89039	Pig growt
30	50	8.5	530	14	ADZ79332	Swine gro
31	50	8.5	530	14	ADZ77169	Pig growt
32	48.8	8.3	2000	8	ADA71938	Rice gene
33	48.2	8.2	1705	4	ABL19005	Drosophil
34	48.2	8.2	1705	13	ADQ89713	Antagonis
35	48.2	8.2	3100	4	ABL18996	Drosophil
36	48.2	8.2	3100	4	ABL19004	Drosophil
37	45.4	7.7	540	12	ADK17120	Nancarchil
38	45.4	7.7	9085	12	ADK16049	Continuation (5 of
39	44.2	7.5	2000	11	ACL37108	Rice stre
40	43.6	7.4	5925	10	ADD29577	Human tum
41	43.6	7.4	5925	14	ADW95930	CDNA enco
42	43.6	7.4	5925	14	ADX15796	DNA encod
43	43.6	7.4	5925	14	ADX25983	Novel cel
44	43.6	7.4	6010	12	ADQ22038	Human sof
45	43.6	7.4	6010	12	ADQ22007	Human sof

ALIGNMENTS

RESULT 1
ADZ89040
ID ADZ89040 standard; DNA; 589 BP.
XX
AC ADZ89040;
XX
DT 28-JUL-2005 (first entry)
XX
DE Pig growth factor III (GF III) gene, seq id 3.
XX
KW Growth; biochip; swine; hog raising; growth factor III; gene; ds.
XX
OS Sus scrofa; Kagoshima Berkshire.
XX
PN US2005112597-A1.
XX
PD 26-MAY-2005.
XX
PF 26-FEB-2004; 2004US-00785981.
XX
PR 24-NOV-2003; 2003KR-00083653.
XX
PA (KIMC//) KIM C.
PA (YEOJ//) YEO J.
PA (LEEJ//) LEE J.
PA (SONG//) SONG Y.
PA (CHOK//) CHO K.
PA (CHUN//) CHUNG K.
PA (KIMI//) KIM I.
PA (JINS//) JIN S.
PA (PARK//) PARK S.
PA (JUNG//) JUNG J.
PA (LEEM//) LEE M.
PA (KWON//) KWON E.
PA (CHOE//) CHO E.
PA (CHOH//) CHO H.
PA (SHIN//) SHIN S.
PA (NAMH//) NAM H.
PA (HONG//) HONG Y.
PA (HONG//) HONG S.
PA (KANG//) KANG Y.
PA (HAYY//) HA Y.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 144.524 Seconds
(without alignments)
7244.353 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttccttaatatgat.....tagtgccattgaatcctgg 589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCPUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528.4	89.7	2703	3	US-09-620-312D-152
2	137	23.3	396	3	US-09-640-173-150
3	137	23.3	396	3	US-09-713-550-150
4	137	23.3	396	3	US-09-825-294-150
5	137	23.3	396	3	US-09-970-966-150
6	48.2	8.2	886	3	US-09-270-767-31527
7	48.2	8.2	1514	3	US-09-270-767-15199
8	48	8.1	1141	3	US-09-806-708B-22
9	43.6	7.4	5925	3	US-09-949-016-5233
10	40.4	6.9	6016	3	US-09-949-016-1054
11	40.4	6.9	6016	3	US-09-949-016-2264
12	39.4	6.7	1428	3	US-09-248-796A-1936
13	39.4	6.7	2082	3	US-09-248-796A-2564
14	38.8	6.6	601	3	US-09-949-016-40750
15	38.8	6.6	462589	3	US-09-949-016-12900
16	38.8	6.6	476044	3	US-09-949-016-12412
17	38.6	6.6	723	3	US-09-134-000C-2397
18	38.4	6.5	9048	3	US-08-973-273-4
19	38.2	6.5	1368	3	US-09-248-796A-11323
20	38.2	6.5	1716	3	US-08-656-034-9
21	38	6.5	1698	3	US-09-248-796A-1623
22	37.8	6.4	822	3	US-09-710-279-607
23	37.8	6.4	2950	3	US-09-710-279-3349
24	37.8	6.4	3760	3	US-09-710-279-4029

Sequence 239, App
Sequence 1000, Ap
Sequence 1071, Ap
Sequence 16353, A
Sequence 1893, Ap
Sequence 2082, Ap
Sequence 14502, A
Sequence 14, Appli
Sequence 26797, A
Sequence 2885, Ap
Sequence 11252, A
Sequence 15845, A
Sequence 2570, Ap
Sequence 2813, Ap
Sequence 3873, Ap
Sequence 1, Appli
Sequence 3017, Ap
Sequence 145280,
Sequence 3, Appli
Sequence 121, App

ALIGNMENTS

RESULT 1

US-09-620-312D-152
; Sequence 152, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Raundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PC-FLGenes Version 1.0
; SEQ ID NO 152
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(2329)
US-09-620-312D-152

Query Match 89.7%; Score 528.4; DB 3; Length 2703;
Best Local Similarity 98.7%; Pred. No. 2.3e+146;
Matches 543; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GTTGTTCCTTTAAATATGATGTTCACCAAGCTGCATTGGAGACTCATTCAGTAATATT 60

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocorelation Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 713 Seconds
(without alignments)
6831.225 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttccttaaatgat.....tagtgcattgaatcctgg 589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	589	9	US-10-785-981-3
2	589	100.0	589	9	US-10-789-723-3
3	589	100.0	589	9	US-10-786-052-3
4	528.4	89.7	1932	9	US-10-745-237-341
5	528.4	89.7	2414	6	US-10-264-237-528
6	528.4	89.7	2703	5	US-10-037-270-152
7	528.4	89.7	2703	6	US-10-117-722-152
8	528.4	89.7	2703	9	US-10-122-851-152
9	391.6	66.5	2734	9	US-10-450-763-20426
10	304	51.6	529	4	US-09-925-065A-278866
11	304	51.6	529	4	US-09-925-065A-278867
12	247	41.9	595	4	US-09-925-065A-278868
13	180.2	20.6	510	3	US-09-783-590-2979
14	137	23.3	396	3	US-09-825-294-150
15	137	23.3	396	3	US-09-970-966-150
16	137	23.3	396	3	US-10-212-677-150
17	137	23.3	396	6	US-10-361-811-150
18	137	23.3	396	6	US-10-369-186-150
19	59.4	10.1	492	3	US-09-918-995-8741
20	59	10.0	1208	9	US-10-450-763-20425
21	51	8.7	469	9	US-10-785-981-4
22	51	8.7	469	9	US-10-789-723-4
23	51	8.7	469	9	US-10-786-052-4

24	50	8.5	530	9	US-10-785-981-2	Sequence 2, Appli
25	50	8.5	530	9	US-10-789-723-2	Sequence 2, Appli
26	50	8.5	530	9	US-10-786-052-2	Sequence 2, Appli
27	48.2	8.2	1705	9	US-10-745-237-143	Sequence 143, App
28	48.2	8.2	1705	10	US-11-097-143-25748	Sequence 25748, A
29	48.2	8.2	3100	10	US-11-097-143-25735	Sequence 25735, A
30	48.2	8.2	3705	10	US-11-097-143-25747	Sequence 25747, A
31	45	7.6	637	4	US-09-925-065A-754045	Sequence 754045,
32	43.6	7.4	5925	8	US-10-335-053-26	Sequence 26, Appl
33	43.6	7.4	6010	8	US-10-723-860-57	Sequence 57, Appl
34	43.6	7.4	6010	8	US-10-723-860-105	Sequence 105, App
35	43.6	7.4	6010	8	US-10-723-860-4827	Sequence 4827, Ap
36	43.6	7.4	6010	8	US-10-723-860-4858	Sequence 4858, Ap
37	42	7.1	555	3	US-09-969-034-466	Sequence 466, App
38	40.4	6.9	5874	9	US-10-450-763-21224	Sequence 21224, A
39	40	6.8	606398	8	US-10-719-993-67882	Sequence 286, App
40	40	6.8	18683	6	US-10-311-455-286	Sequence 34, Appl
41	40	6.8	18683	6	US-10-240-452-34	Sequence 8, Appli
42	40	6.8	495269	7	US-10-398-221-8	Sequence 2058, Ap
43	40	6.8	3011208	7	US-10-398-221-2058	Sequence 151, App
44	39.8	6.8	64482	7	US-10-322-696-151	Sequence 976, App
45	39.6	6.7	8700	6	US-10-311-455-976	

ALIGNMENTS

RESULT 1

US-10-785-981-3
; Sequence 3, Application US/10785981
; Publication No. US20050112597A1
; GENERAL INFORMATION:
; APPLICANT: GYONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
; FILE REFERENCE: 3884-0120P
; CURRENT APPLICATION NUMBER: US/10/785,981
; CURRENT FILING DATE: 2004-06-26
; PRIOR APPLICATION NUMBER: KR 2003-83653
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-785-981-3

Query Match	100.0%	Score 589;	DB 9;	Length 589;
Best Local Similarity	100.0%	Pred. No. 7.6e-148;		
Matches 589;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTGTGTCCTTTAAATATGATGTTGCCACAAAGCTGCATTCAGTAAATATT	60	
Db	1	GTGTGTCCTTTAAATATGATGTTGCCACAAAGCTGCATTCAGTAAATATT	60	
Qy	61	TCCAATGTGCCACCTCAAGAGAGATCTTCAAGTCTTTCTTACTGATGATACATCAAG	120	
Db	61	TCCAATGTGCCACCTCAAGAGAGATCTTCAAGTCTTTCTTACTGATGATACATCAAG	120	
Qy	121	GAAGTAATTCAGCAGTTTCATTTGATGCTCCTGAGTGTAGCAGTCAAGAAACGTTCTTGT	180	
Db	121	GAAGTAATTCAGCAGTTTCATTTGATGCTCCTGAGTGTAGCAGTCAAGAAACGTTCTTGT	180	
Qy	181	TTACCTAGGATGAAACCTCGACAGCAATGAAATTTTAAACCTGTTGATAGAAAGCA	240	
Db	181	TTACCTAGGATGAAACCTCGACAGCAATGAAATTTTAAACCTGTTGATAGAAAGCA	240	
Qy	241	AATGTTGCATCTCTGTTTCTGGGGCATTGATCCATGCTTATTCACCCCTGCTGAC	300	
Db	241	AATGTTGCATCTCTGTTTCTGGGGCATTGATCCATGCTTATTCACCCCTGCTGAC	300	

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioccelexation Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 450.034 Seconds
(without alignments)
2778.314 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgtcccttaatatgat.....tagtgcattgaatcctgg 589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA_New.*
1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	304	51.6	529	6	US-09-925-065A-278866 Sequence 278866
2	304	51.6	529	6	US-09-925-065A-278867 Sequence 278867
3	247	41.9	595	6	US-09-925-065A-278868 Sequence 278868
C	4	45	7.6	637	6 US-09-925-065A-754045 Sequence 754045
5	43.6	7.4	5925	12	US-11-000-688-1358 Sequence 1358, Ap
6	41.2	7.0	2147	8	US-10-750-185-40169 Sequence 40169, A
7	41.2	7.0	2147	8	US-10-750-623-40169 Sequence 40169, A
C	8	39.4	6.7	493	6 US-09-925-065A-301178 Sequence 301178, A
C	9	39.4	6.7	493	6 US-09-925-065A-301179 Sequence 301179, A
10	37.8	6.4	822	8	US-10-793-626-607 Sequence 607, App
11	37.8	6.4	1400	12	US-11-136-527-6340 Sequence 6340, Ap
C	12	37.8	6.4	2950	8 US-10-793-626-3349 Sequence 3349, Ap
13	37.8	6.4	3378	12	US-11-136-527-2244 Sequence 2244, Ap
C	14	37.8	6.4	3760	6 US-10-793-626-4029 Sequence 4029, Ap
15	37.4	6.3	405	6	US-09-925-065A-406315 Sequence 406315, A
16	37.4	6.3	577	6	US-09-925-065A-474125 Sequence 474125, A
17	37.4	6.3	618	6	US-09-925-065A-945465 Sequence 945465, A
18	37.4	6.3	643	6	US-09-925-065A-801427 Sequence 801427, A
19	37.4	6.3	643	6	US-09-925-065A-801428 Sequence 801428, A
20	37.4	6.3	643	6	US-09-925-065A-801429 Sequence 801429, A

21	37	6.3	2222	8	US-10-750-185-46406 Sequence 46406, A
22	37	6.3	2222	8	US-10-750-623-46406 Sequence 46406, A
23	36.8	6.2	519	6	US-09-925-065A-207084 Sequence 207084, A
24	36.2	6.1	6035	12	US-11-136-527-3751 Sequence 3751, Ap
25	36.2	6.1	6052	12	US-11-150-888-13 Sequence 13, Appl
C	26	36	6.1	588	6 US-09-925-065A-623204 Sequence 623204, A
C	27	35.8	6.1	587	6 US-09-925-065A-250166 Sequence 250166, A
C	28	35.8	6.1	1660	8 US-10-750-185-50752 Sequence 50752, A
C	29	35.8	6.1	1660	8 US-10-750-623-50752 Sequence 50752, A
C	30	34.8	5.9	577	6 US-09-925-065A-601955 Sequence 601955, A
C	31	34.8	5.9	1922	6 US-09-925-065A-668701 Sequence 668701, A
C	32	34.8	5.9	1922	6 US-09-925-065A-668702 Sequence 668702, A
C	33	34.8	5.9	1922	6 US-09-925-065A-668703 Sequence 668703, A
C	34	34.6	5.9	574	6 US-09-925-065A-339172 Sequence 339172, A
C	35	34.6	5.9	1160	6 US-09-925-065A-951129 Sequence 951129, A
C	36	34.6	5.9	1617	6 US-09-925-065A-673939 Sequence 673939, A
37	34.4	5.8	575	6	US-09-925-065A-394695 Sequence 394695, A
38	34.4	5.8	2678	6	US-09-925-065A-714439 Sequence 714439, A
39	34.4	5.8	2678	6	US-09-925-065A-714440 Sequence 714440, A
C	40	34.2	5.8	1551	8 US-10-750-185-36922 Sequence 36922, A
C	41	34.2	5.8	1551	8 US-10-750-623-36922 Sequence 36922, A
C	42	34.2	5.8	2292	8 US-10-821-234-767 Sequence 767, App
43	34.2	5.8	3727	12	US-11-091-883-22 Sequence 22, Appl
44	34.2	5.8	3727	12	US-11-091-883-168 Sequence 168, Appl
45	34.2	5.8	190276	8	US-10-661-966-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-925-065A-278866
; Sequence 278866, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278866
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278866

Query Match 51.8%; Score 304; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.2e-68;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTGTGCTTCTTAATATGATGTTGCCACAGCTGCGACTGAGACTCATTCAGTAATATT	60
Db	226	GTGTGCTTCTTAATATGATGTTGCCACAGCTGCGACTGAGACTCATTCAGTAATATT	285
QY	61	TCCAATGTCACCTCAAGAGAGATCTTCAAGTCTTTCTTACTGATGACATGAAG	120
Db	286	TCCAATGTCACCTCAAGAGAGATCTTCAAGTCTTTCTTACTGATGACATGAAG	345
QY	121	GAAGTAATTCAGAGTTCATTTGATGTCGTGAGTGTAGCAAGAACTGCTTGTGT	180

Db 346 GAAGTAATTCAGCAGTTCATTGATGTCCTCAGTGTAGCAGTCAAGAAACGTGCTTGTGT 405
Qy 181 TTACCTAGGATGAAACCTGACAGCAAAATGAAGTTTGTAAACCGTGTGATAGGAAAGCA 240
Db 406 TTACCTAGGATGAAACCTGACAGCAAAATGAAGTTTGTAAACCGTGTGATAGGAAAGCA 465
Qy 241 AATGTTGCAATCCTGTTTCTGGGGGCAATGATCCATGTTATTCGAACCCCTGCTGAC 300
Db 466 AATGTTGCAATCCTGTTTCTGGGGGCAATGATCCATGTTATTCGAACCCCTGCTGAC 525
Qy 301 CGTC 304
Db 526 CGTC 529
RESULT 2
US-09-925-065A-278867
; Sequence 278867, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278867
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278867
Query Match 51.6%; Score 304; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.2e-68;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTTCCTTTAATATGATGTTGCCACAAGCTGCATTTGGAGACTCAATTCAGTAATATT 60
Db 226 GTTGTTCCTTTAATATGATGTTGCCACAAGCTGCATTTGGAGACTCAATTCAGTAATATT 285
Qy 61 TCCATGTGTCACCTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACATCAAG 120
Db 286 TCCATGTGTCACCTCAAGAGAGATATCTCAAGTCTTTCTTACTGATGTACATCAAG 345
Qy 121 GAAGTAATTCAGCAGTTCATTGATGTCCTGAGTGTAGCAGTCAAGAAACGTGCTTGTGT 180
Db 346 GAAGTAATTCAGCAGTTCATTGATGTCCTGAGTGTAGCAGTCAAGAAACGTGCTTGTGT 405
Qy 181 TTACCTAGGATGAAACCTGACAGCAAAATGAAGTTTGTAAACCGTGTGATAGGAAAGCA 240
Db 406 TTACCTAGGATGAAACCTGACAGCAAAATGAAGTTTGTAAACCGTGTGATAGGAAAGCA 465
Qy 241 AATGTTGCAATCCTGTTTCTGGGGGCAATGATCCATGTTATTCGAACCCCTGCTGAC 300
Db 466 AATGTTGCAATCCTGTTTCTGGGGGCAATGATCCATGTTATTCGAACCCCTGCTGAC 525
Qy 301 CGTC 304
Db 526 CGTC 529

RESULT 3
US-09-925-065A-278868
; Sequence 278868, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278868
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278868
Query Match 41.9%; Score 247; DB 6; Length 595;
Best Local Similarity 97.0%; Pred. No. 6.2e-54;
Matches 261; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
Qy 282 TATTGCAACCCCTTGCTGACCGTCATATTCCTTTAGATGAACCAATTGATCTTCTTAATGT 341
Db 1 TATTGCAACCCCTTGCTGACCGTCATATTCCTTTAGATGAACCAATTGATCTTCTTAATGT 60
Qy 342 AGCTTTCTATAGCTGAAGAAAGACCATGCCAATCTTAAACAGAGAGGATATAACA 401
Db 61 AGCTTTCTATAGCTGAAGAAAGACCATGCCAATCTTAAACAGAGAGGATATAACA 120
Qy 402 GAAATAATAATGTGAATACCTTCAGAGAATTCCTCTAAAGATGTTGCTGCTGCTGC 461
Db 121 GAAATAATAATGTGAATACCTTCAGAGAATTCCTCTAAAGATGTTGCTGCTGCTGC 180
Qy 462 TGACAGTCCCTAATAAATACAT-TCAGTGTACAGATCGAATCAGAGAGCGCGGACTAAA 520
Db 181 TGACAGTCCCTAATAAATACATGTCAGTGTACAGATCGAATCAGAGAGCGCGGACTAAA 240
Qy 521 GGAATCTACAAGCTGTTAGCTGATGACCAA 549
Db 241 GGAATCTACAAGCTGTTAGCCCTTCCCGAA 269
RESULT 4
US-09-925-065A-754045/c
; Sequence 754045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 2837.15 Seconds
(without alignments)
9396.598 Million cell updates/sec

Title: US-10-785-981-4
Perfect score: 469
Sequence: 1 cattatgagggtacgcg.....tagtgcattgaaatcctgg 469

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	408.2	87.0	1131	8	CR541796
2	408.2	87.0	1134	11	AY893990
3	408.2	87.0	1374	6	CO714735
4	408.2	87.0	1374	6	CS119314
5	408.2	87.0	1381	6	AX834441
6	408.2	87.0	1381	8	AK096902
7	408.2	87.0	1694	8	BC012597
8	406.6	86.7	1134	8	CR536516
9	406.6	86.7	1374	8	HUMACTASK
10	353.2	75.3	1587	5	AB086240
11	352	75.1	1419	9	MUSACSM
12	351.6	75.0	1568	5	AB021652
13	351.6	75.0	1582	5	AB086242
14	350.4	74.7	1457	9	BC014877
15	350	74.6	1611	5	AB021650
16	348.8	74.4	1518	9	BC061974
17	347.2	74.0	1251	9	MMACTASR
18	347.2	74.0	2472	5	AB052654

19	342.4	73.0	1191	9	MUSACSM
20	337.6	72.0	1134	5	AY690421
21	337.6	72.0	1268	5	CRASAA2
22	336	71.6	1325	5	S63494
23	334.4	71.3	1184	5	AY35870
24	334.4	71.3	1188	5	AY35871
25	334.4	71.3	1260	5	CYISAA1
26	334	71.2	1134	5	AF503593
27	330.8	70.5	1134	5	AF503591
28	328	69.9	1134	5	AF303985
29	328	69.9	1330	4	BT021508
30	327.6	69.9	996	5	AY735013
31	327.6	69.9	1140	5	AY35872
32	327.6	69.9	1401	5	AB086241
33	326.4	69.6	1284	5	AF180887
34	326.4	69.6	1302	5	BC045406
35	326.4	69.6	1316	5	BC065435
36	326.4	69.6	1839	4	OCRAGNMA
37	326	69.5	1400	5	AB021651
38	326	69.5	1436	5	AB021649
39	326	69.5	1555	5	AB037866
40	325.2	69.3	1340	9	MMACTASM
41	325.2	69.3	1354	9	BC064800
42	325.2	69.3	1361	6	AX827826
43	325.2	69.3	1361	9	RNACTAV
44	324.8	69.3	1131	2	AY161281
45	324.8	69.3	1134	5	AF503589

ALIGNMENTS

RESULT 1

CR541796

LOCUS DEFINITION

CR541796 1131 bp mRNA linear PRI 29-JUN-2004
Homo sapiens full open reading frame CDNA clone RZPD0834B0631D for gene ACTAL, actin, alpha 1, skeletal muscle; complete cds, without stopcodon.

ACCESSION

CR541796.1 GI:49456548

VERSION

Full ORF shuttle clone, Gateway(TM), complete cds.

KEYWORDS

Homo sapiens

SOURCE

Homo sapiens

ORGANISM

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

1 (bases 1 to 1131)
Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S., Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

AUTHORS

Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)

TITLE

Unpublished

JOURNAL

2 (bases 1 to 1131)

REFERENCE

Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S., Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

AUTHORS

Direct Submission

TITLE

Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

JOURNAL

RZPD; RZPD0834B0631D, ORFNO 3650

COMMENT

www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834

www.rzpd.de/products/orfclones/

Contact: Inge Airlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available from RZPD;
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu): FLH130947.01L
 This CDS clone is part of a collection of human full ORF clones
 jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been cloned without stopcodon.
 The CDS has been inserted into pDONR201 via a BP Clonase (TM)
 reaction. Additional sequence has been added in front of the start
 codon: att. .AAAAA GCA GGC TCC ACC (ATG).
 The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_001100 (GI:5016087) we did
 not find any amino acid exchanges.
 Clone distribution: http://www.rzpd.de/products/orfclones/.

```

FEATURES
    source
        1. .1131
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="RZPD0834B0631D"
            /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
            /lab_host="DH5Alpha"
            /note="vector: pDONR201, Site_1: attP1; Site_2: attP2"
    gene
        1. .1131
            /gene="ACTA1"
    CDS
        1. .>1131
            /gene="ACTA1"
            /codon_start=1
            /protein_id="CAG46595.1"
            /db_xref="GI:49456549"
            /translation="MCDEETALVCDNGSLVKAGPAGDAPRAVPFSIVGRPRHGG
            VMVGMGQDSYVGDEAQSQRGILTLKYPIDHGIITWDDMEKIWHHTFYNELRVAPEE
            HPTLTPALPNKANREKMTQIMPTFNVPMVAIOAVLSLVASGRTTIGVLDSDGG
            VTHNPVIEGYALPHALRLDLAGRDLTDYLMKILTERGYSFVTTAREIVRDIKEKL
            CYVALDFENEMATASSSLSKSEYELPDGQVITIGNERFCRPETILFQPSFIGMESAGI
            HETYSIMKCDIDIRKDLNANNVMSGTTMYPGIADRMQKEITALAPSTMKIKIAP
            PERKYSVMIGGSILASLSTFQQMWTQKYEAGPSIVHRKCF"

```

ORIGIN

```

Query Match      87.0%; Score 408.2; DB 8; Length 1131;
Best Local Similarity 97.9%; Pred. No. 1.6e-58;
Matches 424; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 CATTATGAGGGCTACGCGCTCGCGCAGCATCGCTGACCTGCGCTGGCGGCGCGCA 60
    |||||
Db 498 CATTATGAGGGCTACGCGCTCGCGCAGCATCGCTGACCTGCGCTGGCGGCGCGCA 557

Qy 61 TCTCAGCAGTACTGCTGATGAAGATCTCTCACTGACGCTGGCTACTCTCTTC-TGACCA 119
    |||||
Db 558 TCTCAGCAGTACTGCTGATGAAGATCTCTCACTGACGCTGGCTACTCTCTTCGTCGAC 617

Qy 120 TGAGCGGAGATCGTGGCGGACATCAAGGAGAGCTGTGCTACGTGGCCCTGGACTTCGA 179
    |||||
Db 618 TGAGCGGAGATCGTGGCGGACATCAAGGAGAGCTGTGCTACGTGGCCCTGGACTTCGA 677

Qy 180 GAACGAGATGCGGACGCGCGCTCTCTCTCTCTCTCGAAAGAGTACGAGCTGCCAGA 239
    |||||
Db 678 GAACGAGATGCGGACGCGCGCTCTCTCTCTCTCTCGAAAGAGTACGAGCTGCCAGA 737

Qy 240 CGGCGAGTCAATCAATCGGCAACGAGCGCTTCGGCTGCCCGGAGAGCGCTCTTCAGACC 299
    |||||
Db 738 CGGCGAGTCAATCAATCGGCAACGAGCGCTTCGGCTGCCCGGAGAGCGCTCTTCAGACC 797

Qy 300 CTCCTTCATCGGTATGAGTGGCGGCGCATTCAGAGACCACTACACAGCATCATGAA 359
    |||||
Db 798 CTCCTTCATCGGTATGAGTGGCGGCGCATTCAGAGACCACTACACAGCATCATGAA 857

Qy 360 GTGTGACATCGACATCAGGAAGGACCTGTATGCGCAACAAACGTCATGTGCGGGGCGCAC 419
    |||||
Db 858 GTGTGACATCGACATCAGGAAGGACCTGTATGCGCAACAAACGTCATGTGCGGGGCGCAC 917

```

```

Qy 420 TGATGACCAAGAG 432
Db 918 GATGTACCCCTGGG 930

RESULT 2
AY893990 1134 bp mRNA linear SYN 16-MAR-2005
LOCUS Synthetic construct Homo sapiens clone FLH130947.01L actin alpha 1
DEFINITION (ACTA1) mRNA, partial cds.
ACCESSION AY893990.1 GI:60832847
VERSION AY893990.1
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1134)
AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
TITLE Cloning of human full-length CDS FLEXGene in
JOURNAL Gateway(TM) recombinational vector system
REFERENCE 2 (bases 1 to 1134)
AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). AttB recombinational sites have been added to
either end of the ORF and directionally cloned using the Gateway
cloning system into pDONR 201. Additional sequences in the clone:
'ACC' before the 'ATG' (corresponding to ribosomal binding site and
Kozak consensus sequences). Each clone is clonally isolated and
full-length sequence-verified.
FEATURES
    source
        1. .1134
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /clone="FLH130947.01L"
            /lab_host="Escherichia coli DH5alpha T1 resistant"
            /note="derived from Homo sapiens first strand cDNA library
            from placenta and brain"
    gene
        1. .>1134
            /gene="ACTA1"
    CDS
        1. .>1134
            /gene="ACTA1"
            /notes="skeletal muscle"
            /codon_start=1
            /transl_table=11
            /product="actin alpha 1"
            /protein_id="AAK37027.1"
            /db_xref="GI:60832848"
            /translation="MCDEETALVCDNGSLVKAGPAGDAPRAVPFSIVGRPRHGG
            VMVGMGQDSYVGDEAQSQRGILTLKYPIDHGIITWDDMEKIWHHTFYNELRVAPEE
            HPTLTPALPNKANREKMTQIMPTFNVPMVAIOAVLSLVASGRTTIGVLDSDGG
            VTHNPVIEGYALPHALRLDLAGRDLTDYLMKILTERGYSFVTTAREIVRDIKEKL
            CYVALDFENEMATASSSLSKSEYELPDGQVITIGNERFCRPETILFQPSFIGMESAGI
            HETYSIMKCDIDIRKDLNANNVMSGTTMYPGIADRMQKEITALAPSTMKIKIAP
            PERKYSVMIGGSILASLSTFQQMWTQKYEAGPSIVHRKCF"

```

ORIGIN

```

Query Match      87.0%; Score 408.2; DB 11; Length 1134;
Best Local Similarity 97.9%; Pred. No. 1.6e-58;
Matches 424; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 CATTATGAGGGCTACGCGCTCGCGCAGCATCGCTGACCTGCGCTGGCGGCGCGCA 60
    |||||
Db 498 CATTATGAGGGCTACGCGCTCGCGCAGCATCGCTGACCTGCGCTGGCGGCGCGCA 557

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 398.012 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-4

Perfect score: 469

Sequence: 1 cattatgagggctacgcg.....tagtgccattgaaatcctgg 469

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	100.0	469	14	Adz89041 Pig growt
2	469	100.0	469	14	Adz79334 Swine gro
3	469	100.0	469	14	Adz77171 Pig growt
4	408.2	87.0	1374	14	Adx25976 Novel cel
5	408.2	87.0	1381	11	Adm02880 Human cdn
6	359	76.5	461	8	Abx49264 Bovine ES
7	350.4	74.7	1446	14	Adz60281 Murine Ac
8	347.2	74.0	1134	13	Adv41171 Rat cardi
9	347.2	74.0	1134	14	Adx26223 Novel cel
10	347.2	74.0	1384	14	Adx25859 Novel cel
11	325.2	69.3	1361	10	AdB53865 Primary r
12	325.2	69.3	1361	11	Adw22181 Rat hepat
13	325.2	69.3	1780	14	Adz60324 Murine Ac
14	312	66.5	1288	12	AdF45416 Human vas
15	312	66.5	1288	12	Adn03844 Antipsori
16	312	66.5	1288	13	Adr24777 Breast ca
17	312	66.5	1288	14	Ady54924 Chronic v
18	312	66.5	1404	4	Aah98660 Human EST
19	308.8	65.8	1275	2	Aat72871 Gamma-smo

20	308.8	65.8	1329	10	ADF76557	Adf76557 Novel hum
21	308.8	65.8	1330	6	ABL62474	ABL62474 Colon ade
22	308.8	65.8	1330	6	ABL69196	ABL69196 Prostate
23	308.8	65.8	1330	6	ABK35532	ABK35532 Gene ACTA
24	308.8	65.8	1330	9	ADB70371	ADB70371 Vascular
25	308.8	65.8	1330	11	ADN95551	ADN95551 Human BEC
26	308.8	65.8	1330	12	ADJ37150	ADJ37150 Human mal
27	308.8	65.8	1330	13	ACN39088	ACN39088 Tumour-as
28	308.8	65.8	1330	14	ADZ26568	ADZ26568 Human smo
29	308.8	65.8	1948	11	ACN90751	ACN90751 Breast ca
30	307.4	65.5	501	6	AAS61617	AAS61617 Lung smal
31	307.2	65.5	561	14	ACL55527	ACL55527 Human col
32	307.2	65.5	1224	8	ACC44347	ACC44347 Gene enco
33	307.2	65.5	1575	6	ABK35123	ABK35123 Human cdn
34	307.2	65.5	1744	12	ADP03041	ADP03041 Human hou
35	307.2	65.5	1744	13	ADS88539	ADS88539 Human hou
36	307.2	65.5	1744	13	ADU60171	ADU60171 Housekeep
37	307.2	65.5	1774	10	ADI62878	ADI62878 Human apo
38	307.2	65.5	1845	13	ADS88823	ADS88823 Nucleotid
39	307.2	65.5	1845	13	ADS88824	ADS88824 Nucleotid
40	307.2	65.5	1845	13	ADS88822	ADS88822 Nucleotid
41	307.2	65.5	1918	6	ABK84502	ABK84502 Human cdn
42	307.2	65.5	1918	14	ADZ26064	ADZ26064 Human gen
43	307.2	65.5	1919	6	ABV94253	ABV94253 Breast ca
44	307.2	65.5	1919	7	ADS99914	ADS99914 Human act
45	307.2	65.5	1919	12	ADP03061	ADP03061 Human hou

ALIGNMENTS

RESULT 1

ADZ89041

ID ADZ89041 standard; DNA; 469 BP.

XX AC ADZ89041;

XX 28-JUL-2005 (first entry)

DE Pig growth factor I (GF IV) gene, seq id 4.

XX Growth; biochip; swine; hog raising; growth factor IV; gene; ds.

XX OS Sus scrofa; Kagoshima Berkshire.

XX PN US2005112597-A1.

XX PD 26-MAY-2005.

XX PF 26-FEB-2004; 2004US-00785981.

XX PR 24-NOV-2003; 2003KR-00083653.

XX PA (KIMC//) KIM C.

XX PA (YEOJ//) YEO J.

XX PA (LEEJ//) LEE J.

XX PA (SONG//) SONG Y.

XX PA (CHOK//) CHOK K.

XX PA (CHUN//) CHUNG K.

XX PA (KIMI//) KIM I.

XX PA (JINS//) JIN S.

XX PA (PARK//) PARK S.

XX PA (JUNG//) JUNG J.

XX PA (LEEM//) LEE M.

XX PA (KWON//) KWON E.

XX PA (CHOE//) CHO E.

XX PA (CHOH//) CHO H.

XX PA (SHIN//) SHIN S.

XX PA (NAMH//) NAM H.

XX PA (HONG//) HONG Y.

XX PA (KANG//) KANG Y.

XX PA (HAYY//) HA Y.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 2778.76 Seconds
(without alignments)
7896.735 Million cell updates/sec

Title: US-10-785-981-4

Perfect score: 459

Sequence: 1 catttatggggctacgcg.....tagtgcattgaaatcctgg 469

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_ges1:*
10: gb_ges2:*
11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	408.2	87.0	483	2	BF826972 RCI-HN003
2	408.2	87.0	524	2	BF769879 RCI-IT001
3	408.2	87.0	583	3	BP316694 BP316694
4	408.2	87.0	872	6	CF552285 AGENCOURT
5	408	87.0	520	8	DR174141 HR0001 I2
6	406.6	86.7	576	5	EX499822 DKFZp779J
7	404.6	86.3	598	3	BP317419 BP317419
8	403.4	86.0	615	7	CR791305 DKFZp468C
9	403.4	86.0	685	7	CN369604 170006000
10	403.4	86.0	1543	4	CR859327 Pongo pyg
11	403.2	86.0	527	2	BF826015 MR2-HN003
12	403.2	86.0	581	3	BP319712 BP319712
13	402.4	85.8	765	7	CR752996 DKFZp468B
14	401	85.5	519	6	CD483530 EST_038 S
15	400.2	85.3	686	6	CD610657 56089031H
16	399	85.1	583	3	BP319352 BP319352
17	392.2	83.6	628	3	BP265037 BP265037
18	391.2	83.4	532	1	AJ710329 AJ710329
19	385.2	82.1	827	2	BF790986 602251034
20	384.2	81.9	585	1	AA180732 ZP43003.1
21	381.8	81.4	634	8	DN413152 DN413152
22	381	81.2	526	3	BP265026 BP265026

23	380.8	81.2	521	8	DN417562
24	380.8	81.2	649	8	DN415842
25	380.2	81.1	667	8	DN433726
26	380.2	81.1	698	8	DN427539
27	380.2	81.1	709	8	DN412198
28	380.2	81.1	714	8	DN411744
29	380.2	81.1	767	8	DN417731
30	380	81.0	691	8	DN417836
31	379.4	80.9	502	8	DN389761
32	379.4	80.9	558	8	DN415214
33	379.4	80.9	562	8	DN415434
34	379.4	80.9	603	8	DN423765
35	379.4	80.9	603	8	DN428163
36	379.4	80.9	606	8	DN413850
37	379.4	80.9	611	8	DN411568
38	379.4	80.9	615	8	CX000458
39	379.4	80.9	621	8	DN427832
40	379.4	80.9	631	8	DN412270
41	379.4	80.9	659	8	DN416947
42	379.4	80.9	660	8	CX008816
43	379.4	80.9	660	8	DN417521
44	379.4	80.9	663	8	DN417551
45	379.4	80.9	665	8	DN384014

ALIGNMENTS

RESULT 1
BF826972

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BF826972 RCI-HN0031-221100-012-h12 HN0031 Homo sapiens cDNA, mRNA sequence. EST 13-JAN-2001
BF826972 GI:12170455
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 483)
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zagor, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RCI&t2=RCI-HN0031-
221100-012-h12&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 483.
Location/Qualifiers
1. .483
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0031"
/note="Organ: head_normal; Vector: puc18; Site_1: SmaI;"

Result No.	Query			ID	Description
	Score	Match	Length		
1	312	66.5	1288	3	Sequence 229, Appl
2	312	66.5	1288	3	Sequence 886, Ap
3	308.8	65.8	1275	2	Sequence 1, Appli
4	308.8	65.8	1312	3	Sequence 1850, Ap
5	308.8	65.8	1330	3	Sequence 2, Appli
6	307.2	65.5	1919	3	Sequence 3553, Ap
7	307.2	65.5	2376	3	Sequence 496, App
8	307.2	65.5	4143	3	Sequence 345, App
9	305.6	65.2	1100	3	Sequence 4538, Ap
10	305.6	65.2	1128	3	Sequence 15, Appl
11	305.6	65.2	1134	3	Sequence 1, Appli
12	304	64.8	1393	3	Sequence 32, Appl
13	294.4	62.8	1489	3	Sequence 730, App
14	294.4	62.8	1793	3	Sequence 8857, Ap
15	294.4	62.8	1814	3	Sequence 5442, Ap
16	294.4	62.8	3128	3	Sequence 373, App
17	284.8	60.7	1131	3	Sequence 1, Appli
18	257.6	54.9	183770	3	Sequence 15494, A
19	253.2	54.0	3240	3	Sequence 4, Appli
20	253.2	54.0	3240	3	Sequence 4, Appli
21	250	53.3	3748	2	Sequence 76, Appli
22	249	53.1	5643	2	Sequence 4, Appli
23	243.2	51.9	1481	3	Sequence 7, Appli
24	238.8	50.9	2994	3	GENERAL INFORMA

Query Match	66.5%	Score 312;	DB 3;	Length 1288;
Best Local Similarity	85.5%;	Pred. No. 1.3e-68;		
Matches 359; Conservative	0;	Mismatches 60;	Indels 1;	Gaps 1;
1	CATTATCAGGGCTACGCGCTGCACGCGCATCATGCGCTGGACCTGCGGGCCGCGA	60		
QY				
575	CATCTATGAGGCTATGCCCTGCCCATGCCATCATGCGCTGGACTTGGCTGGCCGTGA	634		
QY				
61	TCTCACCGACTACCTGATGAAGATCCTCATCTGAGCGTGGCTACTCC-TTCTGACCAACAGC	119		
QY				
635	CCTCAGCGACTACCTCATGAAGATCCTCACAGAGAGAGGCTATTCTTTGTGACCAACAGC	694		
DB				
120	TGAGCGCGAGATCGTGGCGGACATCAAGGAGAAGCTGTCTAGCTGGGCCCTGGACTTCGA	179		
QY				
695	TGAGAGAAATTTGTGCGAGACATCAAGGAGAAGCTGTCTATGTGGCCCTGGATTTTGA	754		
DB				
180	GAACGAGATGGGACGGCGGCTCTCTCTCTCCCTGGAAAAAGAGCTACGAGCTGCCAGA	239		
QY				
755	GAATGAGATGGCCACAGAGCTTCTCTCTCTCTCTGGAGAGAGCTATGAGCTGCCAGA	814		
DB				
240	CGGGCAGGTCATCACCATGGGCAACGAGCGCTTCGCTGCCCGGAGACGCTCTTCCAGCC	299		
QY				

Db 815 TGGCAGGTTATCACCATTGGCAATGAGCGCTTCGGCTGCCGTGAGACCCCTCTTCCAGCC 874
Qy 300 CTCCTTATCGGTATGAGTCGGGGGCAATTCAGGACACCTTCAACAGCATCATGAA 359
Db 875 TTCTTTATTTGGCATGGAGTCGGCTGGAAATTCATGAGACCACTTCAATTCATGAA 934
Qy 360 GTGTGACATCGACATCAGGAGGACCTGTATGCCAACAACGTCATGTGCGGGGSCACCAC 419
Db 935 GTGTGACATTCGATCCGTAGGACTTATATGCCAACAATGTCTCTCTGCGGGGSCACCAC 994

RESULT 2
US-09-949-016-4886
; Sequence 4886, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4886
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4886

Query Match 66.5%; Score 312; DB 3; Length 1288;
Best Local Similarity 85.5%; Pred. No. 1.3e-68;
Matches 359; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
Qy 1 CATTATGAGGGCTACGGCTGCGCGACATCGCCATCATGCGCTGGACCTGGCGGGCCGCGA 60
Db 575 CATCTATGAAGGCTATGCCCTGCCCATGCGCATCATGCGCTGGACTTGGCTGGCGCGTGA 634
Qy 61 TCTCACCAGCTACCTGATGAAGATCTTCACTGAGGCTGGCTACTCC-TTCTGACCAAGC 119
Db 635 CTTCAAGGACTACCTCATGAAGATCTTCAAGAGAGAGGCTTATCTTTGTGACCAAGC 694
Qy 120 TGAGCGGAGATCGTGGCGACATCAAGGAGAGCTGTGCTACGTGGCCCTGGACTTGA 179
Db 695 TGAGAGAGAAATTTGGCGAGACATCAAGGAGAGCTGTGCTATGTGGCCCTGGATTTGA 754
Qy 180 GAACGAGATGGCGAGCGCGCTCTCTCTCTCTCTGAAAGAGCTACGAGCTGCGCAGA 239
Db 755 GAATGAGATGCCACAGCAGCTTCTCTCTCTCTCTGAGAGAGCTATGAGCTGCCAGA 814
Qy 240 CGGGAGGTCTATCACCATCGGCAAGAGCGCTTCCGCTGCCCGGAGAGCTCTTCCAGCC 299
Db 815 TGGCAGGTTATCACCATTGGCAATGAGCGCTTCCGCTGCCCTGAGACCCCTCTTCCAGCC 874
Qy 300 CTCCTTATCGGTATGAGTCGGGGGCAATTCAGGACCACTTCAACAGCATCATGAA 359
Db 875 TTCTTTATTTGGCATGGAGTCGGCTGGAAATTCATGAGACCACTTCAATTCATGAA 934
Qy 360 GTGTGACATCGACATCAGGAGGACCTGTATGCCAACAACGTCATGTGCGGGGSCACCAC 419
Db 935 GTGTGACATTCGATCCGTAGGACTTATATGCCAACAATGTCTCTCTCTGCGGGGSCACCAC 994

RESULT 3
US-08-588-113-1
; Sequence 1, Application US/08588113
; Patent No. 5710003

GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1186
US-08-588-113-1

Query Match 65.8%; Score 308.8; DB 2; Length 1275;
Best Local Similarity 85.0%; Pred. No. 7.9e-68;
Matches 357; Conservative 0; Mismatches 62; Indels 1; Gaps 1;
Qy 1 CATTATGAGGGCTACGGCTGCGCGACATCGCCATCATGCGCTGGACCTGGCGGGCCGCGA 60
Db 549 CATCTATGAAGGCTATGCCCTGCCCATGCGCATCATGCGCTGGACTTGGCTGGCGCGTGA 608
Qy 61 TCTCACCAGCTACCTGATGAAGATCCTCAGTGGCTGGCTACTCC-TTCTGACCAAGC 119
Db 609 CCTCAGGACTACTCTCATGAAGATCTTCAAGAGAGGCTATTCCTTTGTGACCAAGC 668
Qy 120 TGAGCGGAGATCGTGGCGACATCAAGGAGAGCTGTGCTACGTGGCCCTGGACTTGA 179
Db 669 TGAGAGAGAAATTTGGCGAGACATCAAGGAGAGCTGTGCTATGTGGCCCTGGATTTGA 728
Qy 180 GAACGAGATGGCGAGCGCGCTCTCTCTCTCTGAAAGAGCTTACGAGCTGCGCAGA 239
Db 729 GAATGAGATGCCACAGCAGCTTCTCTCTCTCTGAGAGAGCTTATGAGCTGCGCAGA 788
Qy 240 CGGGAGGTCTATCACCATCGGCAAGAGCGCTTCCGCTGCCCGGAGAGCTCTTCCAGCC 299
Db 789 TGGCAGGTTATCACCATTGGCAATGAGCGCTTCCGCGTCCCTGAGACCCCTCTTCCAGCC 848
Qy 300 CTCCTTATCGGTATGAGTCGGGGGCAATTCAGGACCACTTCAACAGCATCATGAA 359
Db 849 TTCTTTATTTGGCATGGAGTCGGCTGGAAATTCATGAGACCACTTCAATTCATGAA 908
Qy 360 GTGTGACATCGACATCAGGAGGACCTGTATGCCAACAACGTCATGTGCGGGGSCACCAC 419
Db 909 GTGTGACATTCGATCCGTAGGACTTATATGCCAACAATGTCTCTCTCTGCGGGGSCACCAC 968

Query Match	100.0%;	Score 469;	DB 9;	Length 469;
Best Local Similarity	100.0%;	Pred. No. 2e-128;		
Matches 469;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CATTATGAGGGCTACGCGTGGCGCACGCCCATCATGCGCTGGACCTGGACCTGGCGGGCCGCGA	60	
Db	1	CATTATGAGGGCTACGCGTGGCGCACGCCCATCATGCGCTGGACCTGGCGGGCCGCGA	60	
Qy	61	TCTCACCGACTACTGATGAAGATCTCTACTGAGCGTGGCTACTCTCTTCTGACACACAGCT	120	
Db	61	TCTCACCGACTACTGATGAAGATCTCTACTGAGCGTGGCTACTCTCTTCTGACACACAGCT	120	
Qy	121	GAGCGCGAGATCGTGGCGGACATCAAGGGAAGCTGTGCTACGTGGGCCCTTGGACTTCGAG	180	
Db	121	GAGCGCGAGATCGTGGCGGACATCAAGGGAAGCTGTGCTACGTGGGCCCTTGGACTTCGAG	180	
Qy	181	AACGAGATGCGCAGCGCCGCTCTCTCTCTCTCTGAAAAGAGTACGAGCTGCCAGAC	240	
Db	181	AACGAGATGCGCAGCGCCGCTCTCTCTCTCTCTGAAAAGAGTACGAGCTGCCAGAC	240	
Qy	241	GGGAGGTATACCATCGGCAACGAGCGCTTCGGTCGCCGGAGAGCGTCTTCCAGCCC	300	
Db	241	GGGAGGTATACCATCGGCAACGAGCGCTTCGGTCGCCGGAGAGCGTCTTCCAGCCC	300	

Result No.	Score	Query Match	Length	DB	ID	Description
1	408.2	87.0	1374	12	US-11-000-688-1361	Sequence 1361, App
2	346.4	73.9	1393	12	US-11-136-527-287	Sequence 287, App
3	315.6	67.3	1400	12	US-11-136-527-7451	Sequence 7451, App
4	315.6	67.3	1414	12	US-11-136-527-3355	Sequence 3355, App
5	308.8	65.8	1330	12	US-11-091-883-89	Sequence 89, App1
6	307.2	65.5	1918	8	US-10-947-249-30	Sequence 30, App1
7	307.2	65.5	1919	8	US-10-909-125-1736	Sequence 1736, App
8	307.2	65.5	2532	8	US-10-821-234-179	Sequence 179, App
9	305.6	65.2	1134	8	US-10-821-234-673	Sequence 673, App
10	296	63.1	1128	12	US-11-139-406-1	Sequence 1, App1
11	296	63.1	1725	12	US-11-139-406-2	Sequence 2, App1
12	292.8	62.4	1802	8	US-10-947-249-39	Sequence 39, App1
13	289.8	61.8	1846	12	US-11-128-061-410	Sequence 410, App
14	289.8	61.8	1846	12	US-11-128-061-3583	Sequence 3583, App
15	289.8	61.8	1846	12	US-11-128-061-3586	Sequence 3586, App
16	289.8	61.8	1846	12	US-11-128-061-3589	Sequence 3589, App
17	289.8	61.8	1846	12	US-11-128-049-410	Sequence 410, App
18	289.8	61.8	1846	12	US-11-128-049-3583	Sequence 3583, App
19	289.8	61.8	1846	12	US-11-128-049-3586	Sequence 3586, App
20	289.8	61.8	1846	12	US-11-128-049-3589	Sequence 3589, App

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 3067.03 Seconds
(without alignments)
9396.598 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507

Sequence: 1 tatatagaacgaatcacgt.....tctgtcggttcagcgcag 507

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	42.4	8.4	2000	6	AX655393 Sequence
C 2	41.4	8.2	4001	2	M23391 Drosophila
C 3	41	8.1	110000	1	Continuation (7 of
C 4	41	8.1	110000	1	Continuation (8 of
C 5	40.4	8.0	79951	8	CP000095_07
C 6	39.8	7.9	2852	6	AL121832 Human DNA
C 7	39.8	7.9	3176	2	CO573420 Sequence
C 8	39.8	7.9	5023	6	AY058690 Drosophila
C 9	39.8	7.9	37841	14	CO573419 Sequence
C 10	39.8	7.9	168471	2	AC017708 Drosophila
C 11	39.8	7.9	231562	2	AC006170 Drosophila
C 12	39.6	7.8	2014	8	AE003767 Drosophila
C 13	39.6	7.8	2453	8	U82827 Human trans
C 14	39.6	7.8	110000	15	BC075791 Homo sapi
C 15	39.6	7.8	129355	8	Continuation (201
C 16	39.6	7.8	176120	5	AC004080 Homo sapi
C 17	39.4	7.8	3512	15	AP005521 Oryza sat
C 18	39	7.7	7218	6	AK110440 Oryza sat
					I66494 Sequence 14

19	38.8	7.7	339	2	AY333202	AY333202 Anopheles
20	38.8	7.7	177086	5	BX470219	BX470219 Zebrafish
21	38.6	7.6	110000	15	AE016819_06	Continuation (7 of
22	38.6	7.6	110000	15	AE016819_07	Continuation (8 of
23	38.6	7.6	214503	14	AC161180	AC161180 Mus muscu
C 24	38.6	7.6	349895	1	BX248359	BX248359 Corynebac
C 25	38.4	7.6	381	2	AY333201	AY333201 Anopheles
C 26	38.4	7.6	110000	1	CR543861_25	Continuation (26 o
C 27	38.4	7.6	210950	9	AC129317	AC129317 Mus muscu
C 28	38	7.5	96081	15	AP004328	AP004328 Oryza sat
C 29	38	7.5	110000	15	AP008212_190	Continuation (191
C 30	38	7.5	158857	15	AP005470	AP005470 Oryza sat
C 31	38	7.5	197714	14	AC128967	AC128967 Rattus no
C 32	37.6	7.4	221952	14	AC098902	AC098902 Rattus no
C 33	37.6	7.4	256796	14	AC099183	AC099183 Rattus no
C 34	37.4	7.4	4186	1	AF199442	AF199442 Methanoco
C 35	37.4	7.4	34892	15	AC156447	AC156447 Volvox ca
C 36	37.2	7.3	230137	9	AC094571	AC094571 Rattus no
C 37	37.2	7.3	233270	14	AC094486	AC094486 Rattus no
C 38	37.2	7.3	347050	1	AL591981	AL591981 Listeria
C 39	37.2	7.3	349980	6	AX641670	AX641670 Sequence
C 40	36.8	7.3	27561	2	CEY66A7AR	AL590342 Caenorhab
C 41	36.8	7.3	42287	14	AC151614	AC151614 Emiliania
C 42	36.8	7.3	43395	2	CEY66A7A	AC032622 Caenorhab
C 43	36.8	7.3	110000	1	AP006627_10	Continuation (11 o
C 44	36.8	7.3	110000	1	BX571966_01	Continuation (2 of
C 45	36.8	7.3	146409	5	CR361548	CR361548 Zebrafish

ALIGNMENTS

RESULT 1
AX655393/C
LOCUS AX655393 2000 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5263 from Patent WO03000898.
ACCESSION AX655393
VERSION AX655393.1 GI:29158207

ORYZA SATIVA
ORYZA SATIVA
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
source
1..2000
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Query Match 8.4%; Score 42.4; DB 6; Length 2000;
Best Local Similarity 11.2%; Pred. No. 0.44;
Matches 40; Conservative 161; Mismatches 157; Indels 0; Gaps 0;

QY	146	CATCCCTTCCTGCTCGATGTTGGCGTGCAGTTATAGGCTGCCAACCCGACATACA	205
DB	449	YMWSMYKCRSMKYAKGKCYGCKWYTCYGYMKWYTYNGSYKSRCYKMYMYKMW	390
QY	206	CACCTTACAGGCACCTTATTAAGTTACATCCAGAGGCTCTGTACACCCCTAAGCAGT	265
DB	389	MYMYSYSSMMTYYYAKYKWKYKRGTMYSYKSKYKYYKYYKYYKYYKYYKYYKYY	330
QY	266	GGCAGTGGTAGCGCTGCCCGCTTACCTGCGCAGTGTGGTCTAGCTCCGCTCAAGC	325
DB	329	KWMRKTKYKRCYCWYATCYWCCYKRGYKRGYKRGYKRGYKRGYKRGYKRGYKRGY	270

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 430.26 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507

Sequence: 1 tatatagaaccgaatcacgt.....tctgtcggtttcagccgcag 507

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	100.0	507	14	ADZ89042 Pig grow
2	507	100.0	507	14	ADZ79335 Swine gro
3	507	100.0	507	14	ADZ7172 Pig grow
C 4	42.4	8.4	2000	8	ADA71938 Rice gene
C 5	41.4	8.2	336	2	AZ00010 Antifreez
C 6	41.4	8.2	336	2	AAX88092 Synthetic
C 7	40.8	8.0	891	11	ACL30038 Rice abio
C 8	39.8	7.9	336	2	AAX88093 Synthetic
C 9	39.8	7.9	2852	4	ABL02625 Drosophil
10	39.6	7.9	5023	4	ABL02624 Drosophil
11	39.6	7.8	1167	6	ABK92192 Prostata
12	39.6	7.8	5643	6	ABK931133 Human pro
C 13	37.2	7.3	2712	8	ACA36793 Prokaryot
C 14	37.2	7.3	110000	6	ABA03041 18 o
15	36.8	7.3	362	14	ADV71137 Huntingto
16	36.8	7.3	204803	12	ADQ97348 Mouse can
C 17	36	7.1	728	6	ABQ68861 Listeria
C 18	36	7.1	1296	6	ABQ67797 Listeria
19	36	7.1	1311	6	ABQ67800 Listeria

C 20	36	7.1	2034	6	ABQ70741	Abq70741 Listeria
C 21	36	7.1	110000	4	AAI99683_16	Continuation (17 o
C 22	36	7.1	110000	6	ABQ69245_19	Continuation (20 o
C 23	36	7.1	319630	6	ABQ67194	Abq67194 Listeria
24	35.4	7.0	539	13	ADX10450	Adx10450 Plant ful
25	35.4	7.0	561	13	ADX34527	Adx34527 Plant ful
26	35.4	7.0	642	13	ADX14288	Adx14288 Plant ful
27	35.4	7.0	856	12	ADM47617	Adm47617 Polynucle
C 28	35	6.9	192	13	ADU02160	Adu02160 Novel hum
C 29	35	6.9	863	6	ABK77958	Abk77958 Bacillus
C 30	35	6.9	2511	10	ADJ92192	Adj92192 Human hai
C 31	35	6.9	9732	5	AAS79690	Aas79690 DNA encod
32	34.8	6.9	3990	14	AE91810	Aeb91810 DNA encod
C 33	34.8	6.9	110000	4	AAI99682_16	Continuation (17 o
C 34	34.8	6.9	218802	14	ADW98820	Adw98820 Human her
35	34.6	6.8	336	2	AZ00010	Aaz00010 Antifreez
36	34.6	6.8	336	2	AAX88092	Aax88092 Synthetic
C 37	34.6	6.8	408	8	ACA38339	Aca38339 Prokaryot
C 38	34.6	6.8	411	8	ACA40379	Aca40379 Prokaryot
C 40	34.6	6.8	1010	5	AAS68262	Aas68262 DNA encod
C 41	34.6	6.8	1167	8	ACA54136	Aca54136 Prokaryot
C 42	34.6	6.8	2466	6	ABS69975	Abs69975 Aspergill
C 43	34.6	6.8	110000	4	AAI99682_07	Continuation (8 of
C 44	34.6	6.8	110000	4	AAI99682_08	Continuation (9 of
C 45	34.6	6.8	110000	4	AAI99683_07	Continuation (8 of
					AAI99683_08	Continuation (9 of

ALIGNMENTS

RESULT 1

ADZ89042

ID ADZ89042 standard; DNA; 507 BP.

XX AC ADZ89042;

XX AC ADZ89042;

DT 28-JUL-2005 (first entry)

DE Pig growth factor I (GF V) gene, seq id 5.

XX KW Growth; biochip; swine; hog raising; growth factor V; gene; ds.

XX OS Sus scrofa; Kagoshima Berkshire.

XX PN US2005112597-A1.

XX PD 26-MAY-2005.

XX PF 26-FEB-2004; 2004US-00785981.

XX PR 24-NOV-2003; 2003KR-00083653.

XX PA (KIMC/) KIM C.

PA (YEOJ/) YEO J.

PA (LEEJ/) LEE J.

PA (SONG/) SONG Y.

PA (CHOK/) CHO K.

PA (CHUN/) CHUNG K.

PA (KIML/) KIM I.

PA (JINS/) JIN S.

PA (PARK/) PARK S.

PA (JUNG/) JUNG J.

PA (LEEM/) LEE M.

PA (KWON/) KWON E.

PA (CHOE/) CHO E.

PA (CHOH/) CHO H.

PA (SHIN/) SHIN S.

PA (NAMH/) NAM H.

PA (HONG/) HONG Y.

PA (HONG/) HONG S.

PA (KANG/) KANG Y.

PA (HAY/) HA Y.

```

PA (ROUJ/) ROU J.
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX
DR WPI; 2005-403340/41.
XX
XX Functional cDNA chip useful for screening and function analysis of growth
PT specific genes according to breeds and tissues of swine, comprises
PT substrate and probe comprising growth specific genes in muscle and fat
PT tissues of swine.
XX
XX Claim 2; SEQ ID NO 5; 8pp; English.
XX
XX The invention relates to a functional cDNA chip (I) for screening and
CC function analysis of growth specific genes according to breeds and
CC tissues of swine, comprises a probe comprising growth specific genes in
CC muscle and fat tissues of swine, and a substrate on which the probe is
CC immobilized. Further disclosed is a kit (KI) useful for screening and
CC functional analysis of growth specific gene according to breeds and
CC tissues of swine, comprising (I) integrated in it, Cys-dCTP or Cys-dCTP
CC bound cDNA from RNA of the tissue to be screened, a fluorescence scanning
CC system, and a computer analysis system. (I) and (KI) are useful for
CC screening and function analysis of growth specific gene according to
CC breeds and tissues of swine. (II) is useful in the swine improvement and
CC breeding of a new breed, and in the hog raising industry. The current
CC sequence represents the pig growth factor V (GF V) gene.
XX
XX Sequence 507 BP; 117 A; 160 C; 120 G; 110 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 507; DB 14; Length 507;
Best Local Similarity 100.0%; Pred. No. 9.1e-153;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATATAGAACCGATACGTACATCGGCTGTGACACAGCAGGCGCAAAACAGGCAACCT 60
Db 1 TATATAGAACCGATACGTACATCGGCTGTGACACAGCAGGCGCAAAACAGGCAACCT 60
Qy 61 AGGAGGTTTAAATAGTATACCGCGCTGACACATACATCTACTACCCGGAACCGG 120
Db 61 AGGAGGTTTAAATAGTATACCGCGCTGACACATACATCTACTACCCGGAACCGG 120
Qy 121 GGACAACTAGGGCTCCGCGCATAGCCATCTCTTCTGTCGTGATGTCGGGCTGCAG 180
Db 121 GGACAACTAGGGCTCCGCGCATAGCCATCTCTTCTGTCGTGATGTCGGGCTGCAG 180
Qy 181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Db 181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Qy 241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGCGCTGAGCGCTTACCTCCGCGCAG 300
Db 241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGCGCTGAGCGCTTACCTCCGCGCAG 300
Qy 301 TGTGGTGTAGCTCCGCTCTTAAGCTTCCCGATAGCGCGCTTTTACACACCATCGG 360
Db 301 TGTGGTGTAGCTCCGCTCTTAAGCTTCCCGATAGCGCGCTTTTACACACCATCGG 360
Qy 361 CGGACTAGACACCGTTGTTGAGCGTTAAGCGTCTATGGTAGAGCTGCGCGGACCGCG 420
Db 361 CGGACTAGACACCGTTGTTGAGCGTTAAGCGTCTATGGTAGAGCTGCGCGGACCGCG 420
Qy 421 TGTAGCCAGCTTACTACATGTTAGTTTCAGCAACCCCTCCCAATCCCGTGTCCCTA 480
Db 421 TGTAGCCAGCTTACTACATGTTAGTTTCAGCAACCCCTCCCAATCCCGTGTCCCTA 480
Qy 481 CTCCAACCTCTGTCGGTTTCAGCCGCGAG 507
Db 481 CTCCAACCTCTGTCGGTTTCAGCCGCGAG 507

```

```

RESULT 2
ADZ79335
ID ADZ79335 standard; cDNA; 507 BP.
XX
AC ADZ79335;
XX
DT 28-JUL-2005 (first entry)
XX
XX Swine growth factor GF-V cDNA for cDNA chip diagnostic method.
XX
XX biochip; screening; EST; expressed sequence tag; probe; muscle;
KW immobilization; gene expression; polymorphism; diagnosis;
KW animal breeding; growth factor; ss.
XX
XX Unidentified.
XX
XX US2005112602-A1.
XX
XX 26-MAY-2005.
XX
XX 27-FEB-2004; 2004US-00789723.
XX
XX 24-NOV-2003; 2003KR-00083651.
XX
XX (KIMC/) KIM C.
PA (YEOJ/) YEO J.
PA (LEEJ/) LEE J.
PA (SONG/) SONG Y.
PA (CHOK/) CHO K.
PA (CHUN/) CHUNG K.
PA (KIMI/) KIM I.
PA (JINS/) JIN S.
PA (PARK/) PARK S.
PA (JUNG/) JUNG J.
PA (LEEM/) LEE M.
PA (KWON/) KWON E.
PA (CHOE/) CHO E.
PA (CHOH/) CHO H.
PA (SHIN/) SHIN S.
PA (NAMH/) NAM H.
PA (HONG/) HONG Y.
PA (KANG/) KANG Y.
PA (HAYY/) HA Y.
PA (ROUJ/) ROU J.
PA (KWAC/) KWACK S.
PA (CHOI/) CHOI I.
PA (KIMB/) KIM B.
XX
XX Kim C, Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;
PI Park S, Jung J, Lee M, Kwon E, Cho E, Cho H, Shin S, Nam H;
PI Hong Y, Hong S, Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;
XX
XX WPI; 2005-371656/38.
XX
XX New cDNA chip comprising a probe capable of detecting marker genes
PT specifically expressed in the muscle and fat tissues of swine, and a
PT substrate, useful for screening and function analysis of swine genes.
XX
XX Claim 9; SEQ ID NO 5; 15pp; English.
XX
XX The invention relates to a cDNA chip for screening and function analysis
CC of swine genes comprising a probe capable of detecting marker genes
CC specifically expressed in the muscle and fat tissues of swine and a
CC substrate on which the probe is immobilized. The invention also includes
CC a kit for screening and function analysis of swine genes comprising the
CC cDNA chip. The cDNA chip is useful for screening and function analysis of
CC swine genes, particularly for comparing genetic expression according to
CC polymorphism interpretation, development of new drugs for disease
CC treatment and disease diagnosis, swine improvement. This sequence

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3003.91 Seconds
(without alignments)
7896.735 Million cell updates/sec

Title: US-10-785-981-5
Perfect score: 507
Sequence: 1 tatatagaaccgaatcacgt.....tctgtcggttcagcgag 507

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	61	12.0	932	5	BX432596	BX432596 BX432596
C 2	41.4	8.2	529	1	AV429458	AV429458 AV429458
C 3	41.2	8.1	670	7	CJ019297	CJ019297 CJ019297
C 4	41.2	8.1	701	3	BP169281	BP169281 BP169281
C 5	41.2	8.1	707	7	CJ016021	CJ016021 CJ016021
C 6	41.2	8.1	794	3	BP144350	BP144350 BP144350
C 7	41.2	8.1	803	8	DN106813	DN106813 1104217 M
C 8	41.2	8.1	830	3	BP156807	BP156807 BP156807
C 9	41.2	8.1	862	7	CJ014151	CJ014151 CJ014151
C 10	41.2	8.1	883	8	DN107179	DN107179 1104601 M
C 11	41.2	8.1	896	9	CC086053	CC086053 CSU-K33r.
C 12	40.8	8.0	1180	8	DN703457	DN703457 CLJ47-F08
C 13	40.2	7.9	649	1	AU296640	AU296640 AU296640
C 14	40.2	7.9	813	7	CO448190	CO448190 MZCCL1009
C 15	39.6	7.8	644	5	BW964713	BW964713 BW964713
C 16	39.6	7.8	692	3	BP153784	BP153784 BP153784
C 17	39.4	7.8	689	6	CF076027	CF076027 Hd mx17 6
C 18	39.2	7.7	490	7	CO975370	CO975370 Bsg9N15F
C 19	39.2	7.7	536	7	CO974837	CO974837 Bsg9N09C
C 20	39.2	7.7	567	7	CO972208	CO972208 Bsg9N15E
C 21	39.2	7.7	578	7	CN868859	CN868859 001202AAO
C 22	39.2	7.7	907	7	CO451557	CO451557 MZCCL1016

C 23	39.2	7.7	1069	7	CK217376	CK217376 FGAS02937
C 24	39.2	7.7	1192	6	CD499604	CD499604 CDA40-C10
C 25	39	7.7	572	8	CX685065	CX685065 yd08g03
C 26	39	7.7	929	8	DN567210	DN567210 93829884
C 27	38.6	7.6	412	6	CD489728	CD489728 T27_D06 T
C 28	38.6	7.6	479	9	BH211305	BH211305 Sml-50622
C 29	38.6	7.6	518	9	AQ977896	AQ977896 RPCI-23-3
C 30	38.6	7.6	704	7	CO452019	CO452019 MZCCL1017
C 31	38.6	7.6	787	7	CO445849	CO445849 MZCCL1007
C 32	38.6	7.6	803	7	CO445036	CO445036 MZCCL1009
C 33	38.6	7.6	837	7	CO446224	CO446224 MZCCL1009
C 34	38.6	7.6	853	7	CO463295	CO463295 MZCCL1503
C 35	38.4	7.6	401	7	CN010492	CN010492 WHE3872_C
C 36	38.4	7.6	448	7	CN010179	CN010179 WHE3867_F
C 37	38.4	7.6	486	7	CF842501	CF842501 p8HB020XE
C 38	38.4	7.6	494	7	CF841197	CF841197 p8HB013xG
C 39	38.4	7.6	495	7	CF851149	CF851149 p8MA018xE
C 40	38.4	7.6	593	7	CF839520	CF839520 p8HB002XH
C 41	38.4	7.6	682	7	CF840809	CF840809 p8HB010xO
C 42	38.4	7.6	688	7	CF864916	CF864916 p8ZS013xG
C 43	38.4	7.6	706	7	CN011313	CN011313 WHE3882_F
C 44	38.4	7.6	715	7	CF851215	CF851215 p8MA018xN
C 45	38.2	7.5	461	7	CV515593	CV515593 0048P0010

ALIGNMENTS

RESULT 1
BX432596
LOCUS BX432596 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone linear EST 04-MAY-2004
DEFINITION CSODP032YF14 3-PRIME, mRNA sequence.
ACCESSION BX432596
VERSION BX432596.1 GI:30779118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 3874.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS08AH009ZB10NPL6c=3874.r.

FEATURES
source

Location/Qualifiers
1..932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODP032YF14"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

```
Query Match      12.0%; Score 61; DB 5; Length 932;
Best Local Similarity 48.8%; Pred. No. 3.8e-07;
Matches 182; Conservative 13; Mismatches 175; Indels 3; Gaps 2;

Qy 130 GGGCTCCGCCATAGACCATCTTTCTTCGTGCGTCGATGTTGCGGGCTGCGATTATAGGGC 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 563 GGGCAGCGCTACTGCTCTCCCAACCTAGACGATGTAGAGCAGGACGCTGAATATGAGC 622

Qy 190 TGCCAAACGGCATACACACTTACCAGCCACTTATTAAAGTTACATCCAGAGGCTCTGT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 623 AGCCTTCGGCTATCACTCCAACTCTGCCTCAACAACCTGAATATACCTCGTAGGCACAGA 682

Qy 250 ACCACCCCTAAGCAGTGGCAGTGTAGCCGCTGCGCTGCCCTTACCTGCGCAGTGTGGTGC 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 683 TCCTCTCATTKCTGAGGTYGAGATGGCGAGCGCCCAATCCCATCGGTGAGAAGAGC 742

Qy 310 TAGCTCCGCTCTAGCTTCCCGCATAGCCGCGCTTTTACACACCATCGCGGACCTAGA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 743 ATGAAGCGACATTCGCAATCCCGTATGCGCGCGCAACAATCTTTCATAGCGCGCCACGT 802

Qy 370 CACGTTGGTTGACGCTAAGCGTCTATGTAGCAGCTGCGGCGACCGCGGTGTAGCCAG 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 803 ATCCAGGGCACCTGCGATAGATWTA-GGATGCTGCYCGGCTTCGTCGGAAGCCYGC 861

Qy 430 CTACTACATGTAGTTTTCAGCAACCAACCTGCCAATACCGCTGTCCCTACTCCAACTC 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 862 AAWAY--CCTWGAATGCAAMCCYKCYTCCAGCCTTCKSHGWDGDTCCCATCWCCTTATC 919

Qy 490 TGTGGGTTTCAGC 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 920 TGTGGGCTWGGC 932

RESULT 2
AV429458/c
LOCUS
DEFINITION AV429458 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
VERSION PL003d03_r 5', mRNA sequence.
KEYWORDS
SOURCE AV429458.1 GI:8584683
ORGANISM Porphyra yezoensis
          Porphyra yezoensis
          Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
          Porphyra.
REFERENCE 1 (bases 1 to 529)
AUTHORS Nikaïdo,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
          Tabata,S.
TITLE Generation of 10,154 expressed sequence tags from a leafy
JOURNAL Gametophyte of a marine red alga, Porphyra yezoensis
PUBMED DNA Res. 7, 223-227 (2000)
COMMENT Contact: Erika Asamizu
          The First Laboratory for Plant Gene Research
          Kazusa DNA Research Institute
          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
          Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
          source
            1..529
              /organism="Porphyra yezoensis"
              /mol_type="mRNA"
              /strain="TU-1"
              /db_xref="taxon:2788"
              /clone="PL003d03_r"
              /clone_lib="Porphyra yezoensis TU-1"
              /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
              XhoI"
ORIGIN
Query Match      8.2%; Score 41.4; DB 1; Length 529;
Best Local Similarity 58.5%; Pred. No. 0.32;
Matches 72; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 130 GGGCTCCGCCATAGACCATCTTTCTTCGTGCGTCGATGTTGCGGGCTGCGATTATAGGGC 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 563 GGGCAGCGCTACTGCTCTCCCAACCTAGACGATGTAGAGCAGGACGCTGAATATGAGC 622

Qy 190 TGCCAAACGGCATACACACTTACCAGCCACTTATTAAAGTTACATCCAGAGGCTCTGT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 623 AGCCTTCGGCTATCACTCCAACTCTGCCTCAACAACCTGAATATACCTCGTAGGCACAGA 682

Qy 250 ACCACCCCTAAGCAGTGGCAGTGTAGCCGCTGCGCTGCCCTTACCTGCGCAGTGTGGTGC 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 683 TCCTCTCATTKCTGAGGTYGAGATGGCGAGCGCCCAATCCCATCGGTGAGAAGAGC 742

Qy 310 TAGCTCCGCTCTAGCTTCCCGCATAGCCGCGCTTTTACACACCATCGCGGACCTAGA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 743 ATGAAGCGACATTCGCAATCCCGTATGCGCGCGCAACAATCTTTCATAGCGCGCCACGT 802

Qy 370 CACGTTGGTTGACGCTAAGCGTCTATGTAGCAGCTGCGGCGACCGCGGTGTAGCCAG 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 803 ATCCAGGGCACCTGCGATAGATWTA-GGATGCTGCYCGGCTTCGTCGGAAGCCYGC 861

Qy 430 CTACTACATGTAGTTTTCAGCAACCAACCTGCCAATACCGCTGTCCCTACTCCAACTC 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 862 AAWAY--CCTWGAATGCAAMCCYKCYTCCAGCCTTCKSHGWDGDTCCCATCWCCTTATC 919

Qy 490 TGTGGGTTTCAGC 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 920 TGTGGGCTWGGC 932

RESULT 3
CJ019297/c
LOCUS
DEFINITION CJ019297 full-length enriched swine cDNA library, adult spleen Sus
          scrofa cDNA clone SPL01C010070 5', mRNA sequence.
VERSION CJ019297.1 GI:54521136
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
REFERENCE 1 (bases 1 to 670)
AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
          Okumura,N., Hamasima,N. and Awata,T.
TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs
          derived from porcine full-length cDNA libraries
JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED 14681463
COMMENT Contact: Hirohide Uenishi
          Animal Genome Laboratory, Genome Research Department
          National Institute of Agrobiological Sciences
          2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
          Tel: +81-29-838-8627
          Fax: +81-29-838-8627
          Email: huenishi@affrc.go.jp
          EST project with full-length enriched cDNA libraries carried out in
          Animal Genome Research Program (Japan) by National Institute of
          Agrobiological Sciences and STAFF-Institute
          Single pass sequencing of clones derived from oligo-capped cDNA
          library
          Vector sequences were eliminated by RepeatMasker version 2002/07/13
          and crossmatch version 0.990319
          Low quality bases were trimmed based on the quality values.
FEATURES
          source
            1..670
              /organism="Sus scrofa"
              /mol_type="mRNA"
              /db_xref="taxon:9823"
              /clone="SPL01C010070"
              /tissue_type="spleen"
              /dev_stage="adult"
              /clone_lib="Full-length enriched swine cDNA library, adult
              spleen"
ORIGIN
Query Match      8.1%; Score 41.2; DB 7; Length 670;
Best Local Similarity 48.3%; Pred. No. 0.39;
Matches 115; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy 262 CAGTGGCAGTGGTAGCGCGCTGCCCGCTTACCTCGCAGTGTGTGCTAGTCCGTCCT 321
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 648 CAGCTTTTGTGGTTCCTCCCTGCTCTTGTCTGTCTGTGATCGTGGTGGCGCTCGGGCT 589

Qy 322 AGCTTCCCGATAGCGCGCTTTTACACCATCGCGGACTAGACACCGTGTGTTG 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 588 CCGCTGCTCGGCTCCGAAGCCTTGGGGCTTTCACCGCGCGCGCGGCGGCGGCGG 529

Qy 382 CAGCGTAAGCGCTCTATGGTAGCAGCTGCGCGCGACCGCGGTGTAGCCAGCTTACATGT 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 124.404 Seconds
(without alignments)
7244.353 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507

Sequence: 1 tatatagaaccgaatcacgt.....tctgtcggttcagccgcag 507

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	41.4	8.2	336	2	US-07-814-220-3
C 2	41.4	8.2	336	2	US-07-812-421-3
C 3	39.8	7.9	336	2	US-07-814-220-4
C 4	39.8	7.9	336	2	US-07-812-421-4
C 5	39	7.7	7218	2	US-08-232-463-14
C 6	36	7.1	4403765	3	US-09-103-840A-2
C 7	34.8	6.9	4411529	3	US-09-103-840A-1
C 8	34.6	6.8	336	2	US-07-814-220-3
C 9	34.6	6.8	336	2	US-07-812-421-3
C 10	34	6.7	1879	2	US-08-403-852D-5
C 11	34	6.7	1879	3	US-08-310-646B-5
C 12	34	6.7	1879	3	US-09-231-818-5
C 13	34	6.7	1879	3	US-09-635-359B-5
C 14	33.8	6.7	1294	3	US-09-312-038-4
C 15	33.8	6.7	1294	3	US-09-850-964-4
C 16	33.8	6.7	2289	3	US-09-312-038-3
C 17	33.8	6.7	2289	3	US-09-850-964-3
C 18	33.6	6.6	1505	3	US-09-270-767-11623
C 19	33.2	6.5	567	4	US-09-605-703B-1299
C 20	33	6.5	336	2	US-07-814-220-4
C 21	33	6.5	336	2	US-07-812-421-4
C 22	32.6	6.4	700	3	US-09-735-271-1138
C 23	32.4	6.4	2689	2	US-08-465-795-2
C 24	32.4	6.4	5589	2	US-08-465-795-1

Sequence 5595, Ap
Sequence 7538, Ap
Sequence 22820, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 7512, Ap
Sequence 1, Appli
Sequence 5303, Ap
Sequence 5536, Ap
Sequence 6394, Ap
Sequence 11950, A
Sequence 12062, A
Sequence 11981, A
Sequence 2, Appli
Sequence 1, Appli
Sequence 8976, Ap
Sequence 5780, Ap
Sequence 890, App
Sequence 165855,

ALIGNMENTS

RESULT 1
US-07-814-220-3/C
; Sequence 3, Application US/07814220
; Patent No. 5925540
; GENERAL INFORMATION:
; APPLICANT: Caceci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,220
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael E.
; REGISTRATION NUMBER: 32,635
; REFERENCE/DOCKET NUMBER: CIT.016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 31..324
US-07-814-220-3

Query Match 8.2%; Score 41.4; DB 2; Length 336;
Best Local Similarity 49.8%; Pred. No. 0.0007;
Matches 105; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 297 GCAGTGTGGTGTAGCTCCGCTTAAGCTTCCCGATAGCCGCGCTTTTACACACCA 356
|||||
Db 248 GCAGTAGCTGGGTAGCTGCCGAGCGCTGCTGCGGTGCGCGAGTTGCTGCCGACGA 189
|||||
QY 357 TCGCGGAGTACACACCGTTGGTTGCAGCGTAAAGCTCTATGTAGTAGCAGTGGGGGACC 416
|||||
Db 188 GCTGCTGCGGTAGCAGCGGTAGCTGCCGACGCGCTGCTGCGGTGCGCGAGTAGTGCC 129
|||||
QY 417 GCCGTGTAGCAGCTTACTATGTTAGTTTTCAGCAACCAACCCTGCCCAATACCGGTGTC 476
|||||
Db 128 GCAGCGCTGCTGCGGTGCGCGAGTAGTGCCGACGCGCTGCTGCGGTGCGCGAGTA 69
|||||
QY 477 CCTACTCCAACTCTGTCGGTTTCAGCGCGAG 507
|||||
Db 68 GCAGCTGCTGCTGCCGCGGTGCGAAGCG 38
|||||

RESULT 3
US-07-814-220-4
; Sequence 4, Application US/07814220
; Patent No. 5925540
; GENERAL INFORMATION:
; APPLICANT: Caceci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,220
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael E.
; REGISTRATION NUMBER: 32,635
; REFERENCE/DOCKET NUMBER: CIT.016
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-814-220-4

Query Match 7.9%; Score 39.8; DB 2; Length 336;
Best Local Similarity 49.3%; Pred. No. 0.0025;
Matches 104; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

LOCATION: 31..324
US-07-812-421-3/c

Query Match 8.2%; Score 41.4; DB 2; Length 336;
Best Local Similarity 49.8%; Pred. No. 0.0007;
Matches 105; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 297 GCAGTGTGGTGTAGCTCCGCTTAAGCTTCCCGATAGCCGCGCTTTTACACACCA 356
|||||
Db 248 GCAGTAGCTGGGTAGCTGCCGAGCGCTGCTGCGGTGCGCGAGTTGCTGCCGACGA 189
|||||
QY 357 TCGCGGAGTACACACCGTTGGTTGCAGCGTAAAGCTCTATGTAGTAGCAGTGGGGGACC 416
|||||
Db 188 GCTGCTGCGGTAGCAGCGGTAGCTGCCGACGCGCTGCTGCGGTGCGCGAGTAGTGCC 129
|||||
QY 417 GCCGTGTAGCAGCTTACTATGTTAGTTTTCAGCAACCAACCCTGCCCAATACCGGTGTC 476
|||||
Db 128 GCAGCGCTGCTGCGGTGCGCGAGTAGTGCCGACGCGCTGCTGCGGTGCGCGAGTA 69
|||||
QY 477 CCTACTCCAACTCTGTCGGTTTCAGCGCGAG 507
|||||
Db 68 GCAGCTGCTGCTGCCGCGGTGCGAAGCG 38
|||||

RESULT 2
US-07-812-421-3/c
; Sequence 3, Application US/07812421
; Patent No. 5932697
; GENERAL INFORMATION:
; APPLICANT: Caceci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,421
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael E.
; REGISTRATION NUMBER: 32,635
; REFERENCE/DOCKET NUMBER: CIT.016
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..324
US-07-812-421-3

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 613.737 Seconds
(without alignments)
6831.225 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507
Sequence: 1 tatatagaaccgaatcacgt.....tctgtcggttcagccgcag 507

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	100.0	507	9	US-10-785-981-5
2	507	100.0	507	9	US-10-789-723-5
3	507	100.0	507	9	US-10-786-052-5
4	123.2	24.3	505	7	US-10-424-599-88182
5	61	12.0	523	7	US-10-424-599-79262
6	48.4	9.5	520	5	US-10-184-644-332
7	48.4	9.5	520	5	US-10-184-634-332
8	39.8	7.9	2852	10	US-11-097-143-1178
9	39.8	7.9	5023	10	US-11-097-143-1177
10	39.6	7.8	5093	7	US-10-424-599-134445
11	39.6	7.8	5643	6	US-10-012-952A-43
12	38.6	7.6	3234	8	US-10-425-115-172916
13	38	7.5	480	8	US-10-425-115-167165
14	38	7.5	675	7	US-10-437-963-1319
15	37.2	7.3	2712	7	US-10-282-122A-24663
16	36.6	7.2	610	7	US-10-437-963-68546
17	36.6	7.2	1888	7	US-10-437-963-73429
18	36	7.1	728	7	US-10-398-221-1694
19	36	7.1	1296	7	US-10-398-221-610
20	36	7.1	1311	7	US-10-398-221-613
21	36	7.1	2034	7	US-10-398-221-3554
22	36	7.1	319630	7	US-10-398-221-7
23	36	7.1	3011208	7	US-10-398-221-2058

C	24	35.8	7.1	653	5	US-10-184-644-402	Sequence 402, App
C	25	35.8	7.1	653	5	US-10-184-634-402	Sequence 402, App
C	26	35.8	7.1	1933	8	US-10-425-115-29072	Sequence 29072, A
C	27	35.4	7.0	539	7	US-10-425-114-5025	Sequence 5025, Ap
C	28	35.4	7.0	561	7	US-10-425-114-17347	Sequence 17347, A
C	29	35.4	7.0	642	7	US-10-425-114-8863	Sequence 8863, Ap
C	30	35.4	7.0	856	6	US-10-310-154-35	Sequence 35, Appl
C	31	35	6.9	863	3	US-09-974-300-5249	Sequence 5249, Ap
C	32	35	6.9	2511	9	US-10-846-374B-51	Sequence 51, Appl
C	33	35	6.9	9732	9	US-10-450-763-15494	Sequence 15494, A
C	34	34.8	6.9	218802	9	US-10-897-508-1	Sequence 1, Appli
C	35	34.6	6.8	408	7	US-10-282-122A-26209	Sequence 26209, A
C	36	34.6	6.8	411	7	US-10-282-122A-28249	Sequence 28249, A
C	37	34.6	6.8	1010	9	US-10-450-763-4066	Sequence 4066, Ap
C	38	34.6	6.8	1167	7	US-10-282-122A-42006	Sequence 42006, A
C	39	34.6	6.8	1599	7	US-10-437-963-57512	Sequence 57512, A
C	40	34.6	6.8	2466	7	US-10-468-250A-74	Sequence 74, Appl
C	41	34.4	6.8	824	3	US-09-966-881-54	Sequence 54, Appl
C	42	34.4	6.8	1062	7	US-10-282-122A-13433	Sequence 13433, A
C	43	34.2	6.7	718	8	US-10-425-115-44833	Sequence 44833, A
C	44	34.2	6.7	752	7	US-10-767-701-8355	Sequence 8355, Ap
C	45	34	6.7	1449	3	US-09-738-626-1597	Sequence 1597, Ap

ALIGNMENTS

RESULT 1
US-10-785-981-5
; Sequence 5, Application US/10785981
; Publication No. US20050112597A1
; GENERAL INFORMATION:
; APPLICANT: GYRONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
; FILE REFERENCE: 3884-0120P
; CURRENT FILING DATE: 2004-06-26
; PRIOR APPLICATION NUMBER: US/10/785,981
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Kegoshima Berkshire
US-10-785-981-5

Query Match	100.0%	Score 507;	DB 9;	Length 507;
Best Local Similarity	100.0%	Pred. No. 2.5e-161;		
Matches 507;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	TATATAGAACCGAATCAGTACACTGGGCTGTACCAAGCAGGCGCCAAACAAAGCAACCT	60	
Db	1	TATATAGAACCGAATCAGTACACTGGGCTGTACCAAGCAGGCGCCAAACAAAGCAACCT	60	
Qy	61	AGGAGGTTTAAATAGGTATACGCGCTGTACACATACATACCTACTACCCGAAACCGG	120	
Db	61	AGGAGGTTTAAATAGGTATACGCGCTGTACACATACATACCTACTACCCGAAACCGG	120	
Qy	121	GGACAACTAGGCTCCGCCATAGCCATCTTTCTTGGTGTGATGTTTGGGGCTGTCAG	180	
Db	121	GGACAACTAGGCTCCGCCATAGCCATCTTTCTTGGTGTGATGTTTGGGGCTGTCAG	180	
Qy	181	TTATAGGGTGTCCAAACCGCCATACACCTTACAGGCACCTTATTAGTTACATCCACGA	240	
Db	181	TTATAGGGTGTCCAAACCGCCATACACCTTACAGGCACCTTATTAGTTACATCCACGA	240	
Qy	241	GGGCTCTGTACCAACCCCTAAGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAG	300	
Db	241	GGGCTCTGTACCAACCCCTAAGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAG	300	

Qy 301 TGTGGTGTAGCTCCGCTCTAAGCTTCCCGATAGCGCGCGCTTTTACACACCATCGG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGTGGTGTAGCTCCGCTCTAAGCTTCCCGATAGCGCGCGCTTTTACACACCATCGG 360
Qy 361 CGGACTAGACACCGCTTGGTGGCAGCGTAAGCGTCTATGTGTAGCAGCTGCGGCGACCGCG 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CGGACTAGACACCGCTTGGTGGCAGCGTAAGCGTCTATGTGTAGCAGCTGCGGCGACCGCG 420
Qy 421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Qy 481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507

RESULT 2
US-10-789-723-5
; Sequence 5, Application US/10789723
; Publication No. US20050112602A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: cDNA chip for screening specific genes and analyzing their
; TITLE OF INVENTION: function in swine
; FILE REFERENCE: YLOP040109US
; CURRENT APPLICATION NUMBER: US/10789, 723
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: KR 2003-83651
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-789-723-5

Query Match 100.0%; Score 507; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATATAGAACCGAATCAGTACACTGGGCTTGACCAAGCAGGCGCCAAACAAAGCAACCT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 TATATAGAACCGAATCAGTACACTGGGCTTGACCAAGCAGGCGCCAAACAAAGCAACCT 60
Qy 61 AGGAGGTTATAAATAGTATACGCGCTGACACATACATACATCTACTACCCGAAACGCGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 AGGAGGTTATAAATAGTATACGCGCTGACACATACATACATCTACTACCCGAAACGCGG 120
Qy 121 GGACAACTAGGGCTCCGCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GGACAACTAGGGCTCCGCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 180
Qy 181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Qy 241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Qy 301 TGTGGTGTAGCTCCGCTTCCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGTGGTGTAGCTCCGCTTCCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 360
Qy 361 CGGACTAGACACCGTGGTGGCAGGTAAGCGTCTATGGTAGCAGCTGCGGCGACCGCG 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CGGACTAGACACCGTGGTGGCAGGTAAGCGTCTATGGTAGCAGCTGCGGCGACCGCG 420
Qy 421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480

Db 421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Qy 481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507

RESULT 3
US-10-786-052-5
; Sequence 5, Application US/10786052
; Publication No. US20050113568A1
; GENERAL INFORMATION:
; APPLICANT: GYEONGSANGNAM-DO
; APPLICANT: Chulwook, KIM
; TITLE OF INVENTION: NOVEL GROWTH RELATED GENES FROM SWINE
; FILE REFERENCE: 3884-0119P
; CURRENT APPLICATION NUMBER: US/10786, 052
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: KR 2003-83652
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire
US-10-786-052-5

Query Match 100.0%; Score 507; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATATAGAACCGAATCAGTACACTGGGCTTGACCAAGCAGGCGCCAAACAAAGCAACCT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 TATATAGAACCGAATCAGTACACTGGGCTTGACCAAGCAGGCGCCAAACAAAGCAACCT 60
Qy 61 AGGAGGTTATAAATAGTATACGCGCTGACACATACATACATCTACTACCCGAAACGCGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 AGGAGGTTATAAATAGTATACGCGCTGACACATACATACATCTACTACCCGAAACGCGG 120
Qy 121 GGAACAATAGGGCTCCGCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GGAACAATAGGGCTCCGCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 180
Qy 181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 TTATAGGCTGCCAACCGCCATACACACTTACAGCCACTTATTAAGTTACATCCACGA 240
Qy 241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GGGCTCTGTACACCCCTTAAGCAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Qy 301 TGTGGTGTAGCTCCGCTTCCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGTGGTGTAGCTCCGCTTCCGCTAAGCCATCCCTTCTCGTCTGATGTGCGGCTGCAG 360
Qy 361 CGGACTAGACACCGTGGTGGCAGGTAAGCGTCTATGGTAGCAGCTGCGGCGACCGCG 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CGGACTAGACACCGTGGTGGCAGGTAAGCGTCTATGGTAGCAGCTGCGGCGACCGCG 420
Qy 421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCCCTGCCAATACCCGTGTCCCTA 480
Qy 481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 CTCCAACTCTGTGGTTTCAGCCGCGAG 507

RESULT 4
US-10-424-599-88182
; Sequence 88182, Application US/10424599
; Publication No. US20040031072A1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 387.381 Seconds
(without alignments)
2778.314 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507

Sequence: 1 tatatagaaccgaatcacgt.....ctctgctgttcagccgcag 507

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA New.*
- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
 - 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.8	6.9	3990	12	US-11-052-554A-520 Sequence 520, App
2	32.2	6.4	2539	12	US-11-136-527-2523 Sequence 2523, App
3	32	6.3	523	6	US-09-925-065A-240456 Sequence 240456, App
4	32	6.3	617	6	US-09-925-065A-461295 Sequence 461295, App
5	32	6.3	993	12	US-11-128-061-930 Sequence 930, App
6	32	6.3	993	12	US-11-128-049-930 Sequence 930, App
c 7	32	6.3	1512	6	US-09-925-065A-62278 Sequence 62278, App
c 8	32	6.3	2223	8	US-10-467-657-6265 Sequence 6265, App
c 9	32	6.3	2539	12	US-11-136-527-215 Sequence 215, App
c 10	31.8	6.3	2479	12	US-11-136-527-3303 Sequence 3303, App
11	31.4	6.2	476	6	US-09-925-065A-472363 Sequence 472363, App
12	31.4	6.2	1090	6	US-09-925-065A-680565 Sequence 680565, App
c 13	31.2	6.2	619	6	US-09-925-065A-874582 Sequence 874582, App
c 14	31.2	6.2	978	8	US-10-793-626-3295 Sequence 3295, App
c 15	31.2	6.2	2993	8	US-10-793-626-4155 Sequence 4155, App
c 16	31.2	6.2	3585	8	US-10-793-626-3521 Sequence 3521, App
c 17	31	6.1	2585	8	US-10-909-125-1963 Sequence 1963, App
c 18	31	6.1	889	12	US-11-136-527-373 Sequence 373, App
c 19	31	6.1	889	12	US-11-136-527-4469 Sequence 4469, App
c 20	31	6.1	2183	9	US-11-072-512-1064 Sequence 1064, App

21	31	6.1	2404	9	US-11-072-512-1740 Sequence 1740, App
22	31	6.1	3921	12	US-11-052-554A-523 Sequence 523, App
c 23	31	6.1	4146	12	US-11-052-554A-522 Sequence 522, App
24	30.8	6.1	454	6	US-09-925-065A-654354 Sequence 654354, App
25	30.8	6.1	454	6	US-09-925-065A-654355 Sequence 654355, App
26	30.8	6.1	1086	12	US-11-052-554A-553 Sequence 553, App
c 27	30.8	6.1	4982	8	US-10-276-233A-17 Sequence 17, App
c 28	30.6	6.0	600	12	US-11-136-527-7399 Sequence 7399, App
c 29	30.6	6.0	735	6	US-09-925-065A-920101 Sequence 920101, App
c 30	30.6	6.0	737	6	US-09-925-065A-925759 Sequence 925759, App
c 31	30.6	6.0	755	6	US-09-925-065A-929143 Sequence 929143, App
32	30.6	6.0	756	6	US-09-925-065A-919830 Sequence 919830, App
33	30.6	6.0	2539	12	US-11-136-527-215 Sequence 215, App
c 34	30.4	6.0	2479	12	US-11-136-527-3303 Sequence 3303, App
c 35	30.2	6.0	610	6	US-09-925-065A-479281 Sequence 479281, App
c 36	30.2	6.0	631	6	US-09-925-065A-737789 Sequence 737789, App
c 37	30.2	6.0	6691	12	US-11-186-284-3 Sequence 3, App
c 38	30	5.9	484	6	US-09-925-065A-827061 Sequence 827061, App
c 39	30	5.9	551	6	US-09-925-065A-536506 Sequence 536506, App
c 40	30	5.9	3064	6	US-09-925-065A-716881 Sequence 716881, App
c 41	29.8	5.9	656	12	US-11-136-527-1651 Sequence 1651, App
c 42	29.8	5.9	656	12	US-11-136-527-5747 Sequence 5747, App
c 43	29.8	5.9	2458	8	US-10-131-826A-387 Sequence 387, App
c 44	29.8	5.9	2818	9	US-11-072-512-1830 Sequence 1830, App
45	29.8	5.9	3240	12	US-11-052-554A-529 Sequence 529, App

ALIGNMENTS

RESULT 1
US-11-052-554A-520
; Sequence 520, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 520
; LENGTH: 3990
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-520

Query Match	6.9%	Score	34.8	DB	12	Length	3990
Best Local Similarity	43.1%	Pred. No.	0.79				
Matches	168	Conservative	0	Mismatches	222	Indels	0
Gaps	0						
Qy	118	CGGGGCAACTAGGCTCGCCATAGCCATCTTCTCTGTCGTCGATGTCGGGCTG	177				
Db	3048	CGAGGCAAGCGCGGCG	3107				
Qy	178	CAGTTATAGGCTGCGCAACCGCCATACACACCTTACCAGCCACTTATTAAAGTTACATCCA	237				
Db	3108	CGGCCACGCGCTGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3167				
Qy	238	CGAGGCGCTGTGTACACCCCTTAAGCAGTGGCAGTGGTAGCGCGCGCGCGCGCGCGCG	297				
Db	3168	TAAACGCGGCG	3227				
Qy	298	CAGTGTGTGTAGCTCGCTCTTCCCGATAGCGCGCGCGCGCGCGCGCGCGCGCGCG	357				
Db	3228	CAGACCG	3287				

```
Qy 358 CGCGGACTAGACACCGTGGTTGTCAGCGTAAGCGTCTATGGTAGCAGCTCGCGGACCG 417
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3288 AGCGGCAACGGCGGACAGCGGCAACGGCGGCAAGCGCTCACCGGAGCGCGGCA 3347
Qy 418 CCGTGTAGCCAGCTTACTACATGTTAGTTTTCAGCAACCAACCTCGCCCAATACCCGTGTTC 477
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3348 CGGTGGACCGCGGACACCGCGCAACGGCGGCAACGGTGGCAACGGCGCCAGTGCGCA 3407
Qy 478 CTACTCCACTCTCTCGTTTCAGCCGAG 507
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3408 CTTGTCACTTCACCTCGTGTGACGCGCGG 3437

RESULT 2
US-11-136-527-2523
; Sequence 2523, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2523
; LENGTH: 2539
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2523

Query Match 6.4%; Score 32.2; DB 12; Length 2539;
Best Local Similarity 48.6%; Pred. No. 4.7;
Matches 85; Conservative 1; Mismatches 89; Indels 0; Gaps 0;

Qy 326 TTCCCCGATAGCCCGCGCTTTTACACACCATCGCGGACCTAGACACCGTTGGTTGAGC 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 TCCCCGACGACCTCCCGGACCCCTTGCTGCGAGCCCTCAGCCTCCGAGCTTCAGCAGCAGC 490
Qy 386 GTAAGCGTCTATGTAGCAGCTCGCGGACCGCGTGTAGCCAGCTTACTACATGTTAGT 445
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
491 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 550
Qy 446 TTACGACCAACCCCTGCCAATACCCGTGTTCCCTACTCCAACTCTGTCGGTTTCA 500
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
551 CCCTGCCTCAGCTTGCCCACTCCAGAGCCAGSTTGTCATCCTGCTGTTGCA 605
```

```
RESULT 3
US-09-925-065A-240456
; Sequence 240456, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 240456
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-240456

Query Match 6.3%; Score 32; DB 6; Length 523;
Best Local Similarity 48.9%; Pred. No. 3.8;
Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 44 CCAAAACAAGCAACCTTAGGAGTTATAAAATAGTATACGCGCTGACACATACATAC 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
286 CAATCCATGCTGAGCTGAGAGTTGAAGGCTGTGCCCTATGCTGGCAGTCTCAAATAAG 345
Qy 104 TCACCTACCCGAACGCGGGACAACTAGGCGTCCGCCATAGCCATCTTCTCTGGTGTGTC 163
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
346 CAGCTAAGAGAGAGAGAAACCTTAGGCTCCAGCAGAGCCCTTCTCTGTGATATA 405
Qy 164 GATGTTGCGGCTGCAGTTATAGGCTGCCAACCGCCATACACACCTTACAGCCA 219
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
406 CCAGCTCAGGATAACTCTGTTAAGAGTCAATTTTGTGAACAAATCTGCAGAGCCA 461

RESULT 4
US-09-925-065A-461295
; Sequence 461295, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 461295
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-461295

Query Match 6.3%; Score 32; DB 6; Length 617;
Best Local Similarity 48.9%; Pred. No. 3.9;
Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 44 CCAAAACAAGCAACCTTAGGAGTTATAAAATAGTATACGCGCTGACACATACATAC 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 CAATCCATGCTGAGCTGAGAGTTGAAGGCTGTGCCCTATGCTGGCAGTCTCAAATAAG 69
Qy 104 TCACCTACCCGAACGCGGGACAACTAGGCTCCGCCATAGCCATCTTCTCTGGTGTGTC 163
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
70 CAGCTAAGAGAGAGAGAAACCTTAGGCTCCAGCAGAGCCCTTCTCTGTGATATA 129
Qy 164 GATGTTGCGGCTGCAGTTATAGGCTGCCAACCGCCATACACACCTTACAGCCA 219
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
130 CCAGCTCAGGATAACTCTGTTAAGAGTCAATTTTGTGAACAAATCTGCAGAGCCA 185

RESULT 5
US-11-128-061-930
; Sequence 930, Application US/11128061
```